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MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Sat Jan 9 09:33:03 1999; masPar time 1049.47 Seconds 1495.136 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: >US-08-704-178-1 (1-712) from US08704178.seq (1 of 4) 712 1 ATGGACCTGCAGCTGACCCA.......GGACCACGGTCACCGTCTCCC
TACCTGGACGTCGACTGGGT...........CCTGGTGCCAGTGGCAGAGG

712

Scoring table: TABLE default Gap 6

Nmatch SID: Dbase 0; Query 0

Searched: 567134 seqs, 1101898692 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: emb155

Database:

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_vi 9:em_bat 11:em_ph 12:em_pl 15:gb_bat 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov 21:gb_pat 22:gb_ph 23:gb_pl1 24:gb_pl2 25:gb_pr1 26:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 30:gb_sts 31:gb_sy 32:gb_un 33:gb_vi

Mean 10.607; Variance 5.121; scale 2.071

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Ouerv				
No.	Score	Match	Match Length DB	3 ID	Description	Pred. No.
⊢	705	99.0	711 2	132406	Sequence 1 from patost	
2	705	99.0	711 31	S39590	anti-erbay immumication	0.000+00
ω	410	57.6	720 21	E13599	DNA encoding a signal	0.000+00
4	375	52.7	720 21		Sequence 2 from patont	0.00e+00
5	363	51.9			Sequence 1 from patent	1 500-091
σ	363	51.0		_	CDNA encoding a monocl	1 500 000
7	283	39.7			Mus musculus rearrance	7 500 511
ω	279	39.2	729 10	_	CDNA encoding an monoc	3 330-307
9	279	39.2			Sequence 3 from natent	
10	271	38.1		_	Mouse hybridoma 2d3 mg	
11	270	37.9		. A36642	Sequence 2 from Patent	1 /00-100
12	270	37.9			Sequence 3 from natent	
13	268	37.6	312 28	S48339	Ig V kappa =anti-idiot	7.55e-198

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			IIIIIIIIII	CACAATGACTTGCAGGGCCACCCCAAGTGTAAGTTACATCCACTGGTATCAGCAGAAGCC	TGCAGGGCCACC	CACAATGACT	61 0	Qy
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ã.	therapeutic and	and	s thereof,	Anti-erbB-2 antibodies, combinations thereof,	B-2 antibodi	Anti-erb	TITLE	
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E kida, T., Yasukawa, K., Imanaka, T. and Tak.

PRODUCTION OF SINCLE-STRAND FV ANTIBODY

PATENT: JP 1997220092-A 2 26-AUG-1997;

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TCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
              TCCGCAGCCTGACATCTGAGGACACTGCAGTCTATTATTGTGCAAG
                                                            AGTTCAAGGACAAGGCCATATTGACTGTAGATAAGTCCTCCAGCACAGGCCTACATGGAGC 607
                                                                                                               AGAGCCTTGAGTGGATTGGAGATATTAATTCTCATAGTGGTGGTATTATCTACAACCAAA 547
                                                                                                                                                                 AGGCTTCAGGATACACATTCACTGACTACAACATGGACTGGGTGAAGCAGAGCCATGGAA 487
                                                                                                                                                                                                                    AATTGCAGCAGTCTGGACCTGAACTGGTGAAGCCTTGGGGCTTCAGTGAAGATACCCTGCA 427
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                                                 AGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATGGAGC
                                                                                                  AGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAA
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PN J5-F
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JP 1997220092-A/2
26-AUG-1997
15-FEB-1996 JP 1996027622
EKIDA TEIJI, YASUKAWA KIYOSHI,
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larity 83.1%;
Conservative
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hypothetical: No;
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Location/Qualifiers
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193 c 190 g 16
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d. No. 0.00e+00;
Mismatches 104;
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                                                                               CTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGC 644
                                                                                                                                                                                                                                                 CAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCCTGC
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                                                                   CTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGC
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Anti-epbB-2 antibodies, combinations
diagnostic uses thereof
Patent: US 5587458-A 2 24-DEC-1996;
Location/Qualifiers
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I32407
  Sequence 1
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Pred. No. 4.82e-291;
1; Mismatches 131;
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                                                                              AAGAAGCAGCCGGAACTGGGTCTACTATG 688
                                                                                                        GAAGCAGAGGCATGGACAAGGCCTTGAGTGGATTGGAAATATTTTATCCTGGTAGTGGTAG
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                                                               AAGGAGGGTTACGGACTGGTACTTCGATG
                                                                                                                             CACAGCCTACATGCACCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTAC
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Shimamura, T., Hamuro, J., Nakazawa, H.,
Takeshita, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-2 receptor
Patent: US 5582826-A 1 10-DEC-1996;
Cocation/Qualifiers
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Pred. No. 1.52e-280;
1; Mismatches 128;
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Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "IMMUNOSUPPRESSIVE AGENT";
Patent number JP 1995313188-A/1, 05
Patent number JP 1995313188-A/1, 05
AJINOMOTO CO INC, SUGAMURA KAZUO,.
OS MUS SP. (MOUSE)
PN JP 195313188-A/1
PD 05-DEC-1995
PN 31-APR-1993 JP 939 94491, 0
PI SAINAMURA TOSHIAKI, HAMURO JUN
PI KANAYAMA YUKA,
PI KANAYAMA YUKA,
PI C12P21/08, A61K39/395, A61K39/39
PC C12W15/13/YC12W15/06,
CC C12P21/08,C12R1:19),(C12P21/0
CC Strandedness: Double;
PH Key Linear Cocation/Qualify
FH Key Linear Cocation/Qualify
FH Source // Ccation/Push
FT source // Ccation/Push
FT source // Ccation/Push
FT mat_peptide 1.732
FT mat_peptide 1.732
// Cproduct="anti-pink"
// Product="anti-pink"
// Pro
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Takeshita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1997 (Rel. 52, Created)
08-OCT-1997 (Rel. 52, Last updated, Version cDNA encoding a monoclonal antibody against receptor gamma chain.
JP 1995313188-A/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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  352
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JP 1995313188-A/1
05-DEC-1995
21-APR-1994 JP 1994082836
21-APR-1993 JP 93P 94491, 0
SHIMAMURA TOSHIAKI, HAMURO JUN
                                                                                                                                                                                                                                                                                                                 CGGTGCTGGGACCAAGCTGGAGCTCAAAGTCGACAAATCCTCAGGATCTGGCTCCGAATC
                                                                                                                                                                                                                                   CCCAGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCAGCAGCAT
TGAAGGTAAAGGTGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTC
                                    CAAAAGCACGCAGGTCAAACTCGAGGAGTCTGGATCTGAGCTGGTGAGGCCTGGAGCTTC
                                                                             CGGAGGGGGGTCCAAGCTGGAAATAAAAGGTT-CTA--CCTCTGGTTCTGGTAAATCTTC
                                                                                                                                                         GGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAGTATCATCGTTCCCCGGCTCACGTT
                                                                                                                                                                                                                                                                                                                                                                                               CACCATGACCTGCACTGCCAGCTCAAGTGTAAGTTCCAGTTACTTGCACTGGTACCAGCA 119
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SUGAMURA KAZUO, TAKESHITA TOSHIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C12P21/08, C12R1:19), (C12P21/08, C12R1:91), (C12N1/21, C12R1:19);
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12N15/13//C12N15/06,
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Similarity 79.8%;
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BP; 180 A; 204 C; 182 G; 166 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hamuro J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="anti-IL-2 receptor gamma chain"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus sp."
/cell_type="hybridoma"
/cell_line="GP-2"
1. .732
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Pred. No. 1.52e-280;
1; Mismatches 128;
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human
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KEYWORDS
SOURCE
ORGANISM
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MEDLINE
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                                                Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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GAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCCTGCAAGACTTCTGGTTACTCATTC 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus r
mRNA, partial
U37860
                                                                                                                                                                                                                                                                                          Submitted (10-OCT-1995) Jennifer R. Swartzentruber, Institute, 3601 Spruce St., Philadelphia, PA 19104, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                and
J.
                                                                                                                                                                                                                                                                                                                                                                                                        Activation and negative of antibody-secreting ce
                                                                                                                                                                                                                                                                                                                                                                                                                               Caton,A.J., Swartzentruber,J.R.,
Stark,S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g1127634
                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 336)
Swartzentruber, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinae; Mus.
1 (bases 1 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes;
Vertebrata; Eutheria; Rodentia; Sciurc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                     96136744
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                                              h 39.7%;
Similarity 95.1%;
309; Conservative
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d_a neo-self antiger
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                                                                                                         TTVŢVSSAKT"
                                                                                                                                /product="rearranged immunoglobulin heavy chain variable region"
/region"
/db_xref="pID:g1127635"
/translation="ELVKPGASWKISCKASGYSFTGYTMNWVKQSHGKNLEWIGLINP YUGGTSYNQKFKGKATUTVDKSSSTAYMELLSLTSEDSAVYYCAREWLLRYFDVWGAG
                                                                                                                                                                                                                    /cell_type="B-lymphocyte"
                                                                                                                                                                                                                                 /db_xref="taxon:10090"
                                                                                                                                                                                                                                                        /organism="Mus musculus"
/isolate="h922-163"
                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                              /strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 bp s rearranged al cds.
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                                                Mismatches
                                                         283; DB 28;
No. 7.59e-211;
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                                                                                                           78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa;
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USA
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                                                    Query Match
Best Local S
Matches 48
                                                                                                                                                                                                              Pattent number JP 1995313188-A/2, 05
AJINOMOTO CO INC, SUGAMURA KAZUO...
OS MUS SP. (mouse)
PN JP 1995313188-A/2
PD 05-DEC-1995
PN JP 1995313188-A/2
PD 05-DEC-1995
PF 21-APR-1994 JP 1994082836
PR 21-APR-1994 JP 1994082836
PR 21-APR-1994 JP 399491, 0
PI SHIMAMURA TOSHIAKI, HAMURO JUN
PI KANAYAMA YUKA,
PI SUGAMURA KAZUO, TAKESHITA TOSH
PC C12P21/08,A61K39/395,A61K39/39
PC C12N15/13//C12N15/06,
PC (C12P21/08,C12R119),(C12P21/0
PF (C12P21/08,C12R119),(C12P21/08),(C12R119),(C12P21/08),(C12R119),(C12P21/08),(C12R119),(C12P21/08),(C12R119),(C12P21/08),(C12R119),(C12P21/08),(C12R119),(C12P21/08)
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CDNA encoding an monoclonal antibody against receptor gamma chain.
JP 1995313188-A/2.
Mus sp.
Enter-
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E10362;
E10362;
d1108699
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Takeshita T.;
"IMMUNOSUPPRESSIVE AGENT";
                                                                                                                            Sequence 729
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ATGGATATTCTGCTGACACAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGT-
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C12P21/08,A61K39/395,A61K39/395,C12N1/21,C12N5/20,
C12N15/13//C12N15/06,
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Location/Qualifiers
                                                                                                                            /organism="Mus sp."
199 A; 169 C; 182
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                                                                                                                                                                                                                                       /organism="Mus sp."
/cell_type="hybridoma"
/cell_line="GP-4"
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94491, U.
WIRO JUNJI, J
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                                                      ATGGATATTCTGCTGACACAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGT- 59
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                                                                                                                                                                                                                                                                                                         Sequence
I31036
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Shimamura, T., Hamuro, J., Nakazawa, H.,
                                                                                                                                                                                                                                                                           Unknown
                                                                                                                                                                     interleukin-2 receptor
Patent: US 5582826-A 3 10-DEC-1996;
Location/Qualifiers
                                                                                                                                                                                                                   Takeshita, T
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Pred. No. 2.23e-207;
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89094248
                                                                                                                                                                                         Meek,K., Hasemann,C., Pollok,B., Alkan,S.S., Brait,M., S
Urbail,J. and Capra,J.D.
Structural characterization of antildiotypic antibodies.
that Ab2s are derived from the germline differently than
                                                                                                                                                                     that Ab2s are derived from the germline J. Exp. Med. 169 (2), 519-533 (1989)
                                                                                                                                                                                                                                                                                                                      Submitted (09-JAN-1989) K. Meek, University of Texas Southwestern Medical School, 5323 Harry Hines Blud. Microbiology, Dallas Texas
                                                                                                                                                                                                                                                                                                                                                                Meek,K.
Direct Submission
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/cell_line="Hybridoma 2D3-K"
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                                                            /organism="Mus musculus"
/strain="Balb/c"
                                     /db_xref="taxon:10090"
                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 bp
ma 2d3 п
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   eukaryotes; Metazoa;
entia; Sciurognathi; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                Myomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1995
light chain '
                                                                                                                                                                                                                                                         Slaoui, M.,
                                                                                                                                                                                           Evidence
Abls
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/gene="IG kappa light chain" /note="variable region" /product="IG kappa light chain"

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RESULT 11
LOCUS
DEFINITION
ACCESSION
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ORIGIN
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                                                                                                                                                                                   AUTHORS
TITLE
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Best Local Similarity 94.8%;
Matches 290; Conservative
                                                                                                                                                                     JOURNAL
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                                                                       1 (bases 1 to 315)

Seemann,G. and Bosslet,K.

Antigranulocyte antibody construct, present ED 058570-A 2 09-MAR-1994;

BEHRINGWERKE AG (DE)
Other publication JP 6205693 940726
Other publication CA 2101868 940210
Other publication AU 4441393 940210
Other publication DE 425853 940210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTGGATTICTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCAGCTCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCAAAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAAAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTACTGCCACCAGTGGAGTAGTAACCCCCCAACGTTCGGAGGGGGGACCAAGCTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATTACTGCCAGCAGTGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAA
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                                                                                                                                                                                                                                        Mus musculus
Eukaryotae; mitochondr
Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                       Sequence 2 from A36642
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                                                                                                                                                                                                                                Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="IG kappa light chain"
/db_xref="piD:q938245"
/db_xref="piD:q938245"
/translation="QiPiSQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPK
PWISATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCHQWSSNPPTFGGGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <1. .>321
/gene="IG kappa light chain"
/note="variable region"
/evidence=experimental
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_type="hybridoma/myeloma"
                                                          Location/Qualifiers
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/note="variable region"
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                                                                                                                                                                                                                                           mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                     15 bp DNA
Patent EP0585570
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No. 1.91e-200;
Mismatches 14;
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                                                                                                                                                                                  preparation
                                                                                                                                                                                                                                                                                                                                                                     PAT
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RESULT 12
LOCUS
DEFINITION
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AUTHORS
TITLE
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FEATURES
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SOURCE
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Best Local s
Matches 29
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Best Local s
Matches 29
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Local Similarity 93.3%;
hes 294; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCCTCCCCAAACCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCG
AGATGCTGCCACTTATTACTGCCAGCAGTGGAGTAGTAACCCGCTCACGTTCGGGTGCTGG
                                         CTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCATCAGAGTGGAGGCTGA 239
                                                                                                               AATGACTTGCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGG 123
                                                                                                                          AATGACTTGCAGGGCCAGCTCAAGTGTAAGTTACATGCACTGGTACCAGCAGAAGCCAGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACCAAGCTGGAGAT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGATGCTGCCACTTATTACTGCCAGCAGTAGGAGTAGTAACCCGCTCACGTTCGGTGCTGG
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                                                                        ATCCTCCCCCAAACCTTGGATTTATACCACCTCCAACCTKGCTTCTGGAGTCCCTGCTCG
                                                                                   ATCCTCCCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCG
                               CTTCAGTGGCGGTGGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTGA
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
151657
                                                                                                                                                                                                                                                                                 l (bases 1 to 315)
Seemann,G. and Bosslet,K.
Granulocyte-binding antibody constructs,
Patent: US 5645817-A 3 08-JUL-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   Unknown
                                                                                                                                                                                                                                                                                                                                                             Unknown
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                                                                                                                                                                                                                                                                                                                                        Unclassified.
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larity 93.3%;
Conservative
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Pred.
1; M
                                                                                                                                                                                                Score 270; DB 21;
Pred. No. 1.40e-199;
1; Mismatches 19;
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RESULT 13
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AUTHORS
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JOURNAL
MEDLINE
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Best Local :
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                      254
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 304
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                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                     TGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGT-CACAATGACTTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACCAAGCTGGAGAT 314
GAAATCAAA 312
                                   ACTTATTACTGCCAGCAGTGGAGTAGTAACCCATGGACGTTCGGTGGAGGCACCAAGCTG 303
                                                                GGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTGCC
                                                                            AGTGGGTCTGGGACCTCTTACTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCC
                                                                                                            AAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGC
                                                                                                                       AAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGC 183
                                                                                                                                                          AGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCC
                                                                                                                                                                       AGGGCCAGCTCAAGTGTAAGTTACATGCACTGGTACCAGCAGAAGCCAGGATCCTCCCCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCAAGCTGGAAAT 318
                     ACTTATTACTGCCAGCAGTGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGTCCAAGCTG
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entry [NCBI gibbsq 118382] from the original journal article.
This sequence comes from Fig. 5.
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Molecular cloning of murine monoclonal anti-idiotypic
J. Immunol. Methods 155 (1), 77-89 (1992)
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/translation="VMTQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPKPW
IYATSNLASGVPARESGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPWTFGGGTKLE
                                                                                                                                                                                                                                                                                                                                                                                        /gene="Ig V<kappa>"
/note="anti-idiotypic Fab;
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/gene="Ig V<down>&kgr;</down>"
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/db_xref="taxon:10095"
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/strain="Balb/c"
/db_xref="taxon:10090"
/cell_line="hybridoma"
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 318)

Sandstrom,P., Johansson,A., Ullen,A., Behravan,G. and Stigbrand,T.

Differences in sequence and affinity between three monoclonal anti-idiotypic antibodies against one anti-placental alkaline phosphatase idiotypic antibody
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Sandstrom,P., Johansson,A., Ullen,A.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="monoclonal antibody aH7:38 IgG1 light chain"
/db_xxef="PID:g3044132"
/db_xxef="PID:g3044132"
/translation="DIOLTOSPAILSASPGEKVSMTCRASSSVSYIHMYQQKPGSSPK
PWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSGNPLTFGAGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="anti-idiotypic antibody against anti-placental
alkaline phosphatase antibody; variable region"
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Pred. No. 7.55e-198;
1; Mismatches 22;
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ATAAAAGGT 325
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Parslow,T.G., Blair,D.L., Murphy,W.J. and Granner,D.K.
Structure of the 5' ends of immunoglobulin genes: A novel conserved
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C-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa.
Mouse 702/3 cell DNA.
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1003. .>1337
/note="Ig kappa chain variable region"
/number=2
/number=2
1338. .>1369
/note="kappa cds intron J-C"
/note="kappa cds intron J-C"
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/translation="MDFQVQIPSFLLISASVIMSRGQIVLSQSPAILSASPGEKVTMT
CRASSSSYSYMMYQOKPGSSPKPWIYATSNLASGVPARFSGSGSGTSYSLTISRVEAE
DAATYYCQQWSSNPRTFGGGTKLEIK"
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/db_xref="taxon:10090"
<776. .824
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                                                                   ce encoding the single chain chain anti-erbBl antibody;
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711; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of tumour cells which overexpress the erbB-2 gp185 of breast, ovarian and non-small cell lung carcinomas, coupled to a cytotoxic agent, to treat such tumours. 711 BP; 175 A; 182 C; 189 G; 164 T;
                                                            antibody;
U08545.
US-906555.
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/*tag= a
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WPI; 94-025878/
P-PSDB; R45442.
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Sequence 711 BP; 175 A; 183 C; 187 G; 165 T;
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Example; Fig
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           tacggactggtacttcgatgtctgggggcgcaggggaccacggtcaccgtctcc
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llarity 99.6%;
Conservative
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nich recognise different
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RESULT 3 ID T17728

standard;

CDNA;

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14-MAR-1996.
14-SAUG-1995; U10740.
06-SEP-1994; US-301339.
06-JUN-1995; US-468252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibition of proliferation or survival of, esp. malignant erbB2, cells - by introducing nucleic acid mol. encoding antibody homologue which is expressed and binds, pref. erbB2, protein intracellularly claim 42: Page 29-30; 48pp; English.

A nucleic acid comprises a first sequence encoding a signal peptide (R94019) linked to a second sequence (T17728) encoding a single chain Fv fragment (R94020) that binds a human erbB2 oncoprotein. The anti-erbB2 sFv portion is obtained by PCR using e33sCFv plasmid as template. The signal peptide directs the scFv to the endoplasmic reticulum. The nucleic acid is incorporated into a plasmid or viral vector to facilitate expression of the scFv antibody homologue within e.g. an epithelial carcinoma cell. Intracellular expression of the homologue inhibits surface expression of erbB2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Curiel DT, Deshane J; WPI; 96-171307/17.
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Curiel DT, Deshane J;
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21-MAY-1996 (first entry)
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ody homologue; single chain antibody;
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                                                                                                                                                                                                                                                                                                                                                                                           Producing single chain Fv antibody in Escherichia coli - by expression in an inclusion body, followed by protein folding or by co-expression with a chaperonin as a soluble fraction co-expression with a chaperonin as a soluble fraction co-expression with a chaperonin as a soluble fraction color of the sequences given in T91614-15 encode single chain Fv (scFv) cantibodies which are produced in E. coli. The scFv's are derived from an anti-T3 antibody or an anti-T9130 antibody and are produced cither by: (1) expression as an inclusion body, followed by folding (i.e. by denaturation and solubilisation) or (2) expression as a soluble fraction by co-expression with chaperonin. Using the methods, scFv can be produced in E. coli, either in a soluble fraction or in inclusion bodies. Like the parent double chain antibodies, the scFv polypeptides are useful in immunological diagnosis or for separation and purification, but they lessen the side effects caused by antibody constant regions. The availability of scFv polypeptides contributes
                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding an anti-gpl30 antibody derived scFv. Single chain Fv; scFv; antibody; E. coli; anti-T3 ar anti-gpl30 antibody; inclusion body; chaperonin; ds.
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                                                                                                                                                                                                                                                                                                                                                                      drugs.
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WPI; 97-474306/44.
P-PSDB; W25784.
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15-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                    ccacttattactgccagcagtggagtactaacccgctcacgttcggtgctgggaccaagc
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                                                                                                                                                           GCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTG
                                                                                                                                              CCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTG
                                                                                                                                                                                                                                                                                                      l Similarity
537; Conser
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llarity 83.1%;
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                                                                                                                                                                                                                                                                                                      Score 410; DB 34; 1
Pred. No. 1.02e-272;
1; Mismatches 104;
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                                                                                                                                                                                                                                                                                                                                                                                 of diagnostic and therapeutic
                                                                                                                                                                                                                                                                                                                                                           190 G;
                                                                                                                                                                                                                                                                                                                             Length 720;
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                                                                                                                                                                                              Fig. 1. Single chain antibodies specific for erbB-2 protein, gp185 - with abels or cytotoxin, useful for detection and treatment of tumour cells expressing this protein

Fig. 2. Example 9: Columns 27-30: 28pp: English.

The present cDNA sequence codes for a claimed single-chain antibody, compared e21(Fv), which binds to erbB-2. Monoclonal antibody e21

Cate signated e21(Fv), which binds to erbB-2 cells overexpressing the gp185 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-crbB-2 coding for the heavy- and light-chain antibody as isolated and converted to cDNA. Regions coding for the heavy- and light-chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide claim of tumour cells which overexpress the erbB-2 gp185 composis of tumour cells which overexpress the erbB-2 gp185 compared to a cytotoxic agent, to treat such tumours.

So Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5587458-A.
24-DEC-1996.
07-OCT-1991; 772270.
07-CT-1991; US-772270.
30-JUN-1992; US-906555.
14-MAY-1999; US-61092.
(ARON-) ARONEX PHARM INC.
Bird RE, Kasprzyk PG, Ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T65007 stand
T65007;
T65007;
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Single-chain anti-erbB2 antibody e21(Fv) cDNA.
Single-chain antibody; variable region; light chain; heavy
breast cancer; ovarian cancer; non-small cell lung carcinon
immunodiagnosis; treatment; cytotoxic agent; erbB-2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; W15186
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TGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATG
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                                                                                                      h 52.7%;
Similarity 79.3%;
511; Conservative
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Pred.
1; N
                                                                                                                           375;
No. 4.
                                                                                                   Mismatches
                                                                                DB 25,
4.34e-247;
~hes 131;
                                                                                                                                                 Length
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RESULT RESULT PERSONAL CONTROL OF STREET PERSONA
Example; Fig 8; 37pp; English.

S Example; Fig 8; 37pp; English.

C The source of human erbB-2 protein for the prodn. of antibodies no. 22 and 21 (055180/R45442; Q55181/R45443) is a NIH/3T3 cell

C engineered to express the human erbB-2 protein on its surface (N/CC erbB-2). Abs no. 21 and 23 are directed against the extracellular CC domain of gp185 erbB-2. Nude mice manipulated to produce rapidly CC growing tumours were used in a trial of the efficacy of the Abs. If CC engineesed after 11 days.

CC regressed after 11 days.

CC regressed after 11 days.

CC sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
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(MOLE-) MOLECULAR ONCOLOGY I

Kasprzyk PG, King CR;

WPI; 94-02587R/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-1994.
21-OCT-1992;
30-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoding the single chair Single chair anti-erbBl antibody; monoclonal antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q55181 standard;
Q55181;
                                                                                                                                                                                                                                                                                                      Treatment of malignancies over-expressing ERB-[2 - using and 2 monoclonal antibodies which recognise different epitopes
                                                                                                                                                                                                                                                                                                                                                     WPI; 94-025878/
P-PSDB; R45443.
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W MAb; monoclonal antibody; fybridoma; in
W Fv; antibody variable region; GP-2; Fv(
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Matches
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EP-621338-A.
26-OCT-1994.
21-APR-1994; 106257.
21-APR-1993; JP-094491.
07-MAR-1994; JP-036065.
                                                                                                                              Hamura J,
Takeshita
  Immunosuppressant polypeptide interleukin-2 response Claim 17: Page 29; 37pp; Engl: MAb capable of binding to the
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MAB; monoclonal antibody; hybrid FV; antibody variable region; GI
  Mus sp.

EP-621338-A.

26-OCT-1994.

21-APR-1994;

21-APR-1993;

07-MAR-1994;
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; 106257. ; JP-094491. ; JP-036065.

hybridoma; interleukin-2;

GP-4;

Fv(GP-4);

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Query Match
Best Local S
Matches 55
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Sequence 732 BP; 180 A; 204 C; 182 G; 166 T
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                                                          CACAGCCTACATGGAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGC
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                                                                                                                                                                                                                                         AATGAAGATATCCTGCAAGACTTCTGGTTACTCACTGGCCACACCATGAACTGGGT
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l similarity 79.8%;
550; Conservative
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1; Mismatcl
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d. No. 2.58e-238;
Mismatches 128;
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Matches
                                                      T31541;
18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunosuppressant polypeptide - has ability to block interleukin-2 response
Claim 18; Page 29; 37pp; English.
MAb capable of binding to the gamma chain of the IL-2 receptor, and thus of blocking the IL-2 response, is produced by mouse hybridoma line GP-4 (FERM BP-4640). DNA encoding the variable region of this MAb was expressed in E. coll, yielding Fv(GP-4) with immunosuppressive activity.

Sequence 729 BP; 199 A; 169 C; 182 G; 179 T;
       3H1 heavy chain variable region cDNA.
Anti-idiotype; monoclonal antibody; MAb; 3H1; CEA; carcinoembryonic antigen; cancer; gene therapy; im vaccine; genetic immunisation; heavy chain; VH; ss
                                                                               T31541
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                                                                                                                          AGCCTACATGGAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
                                                                              standard;
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CC (A cDNA clone (T31541) codes for the heavy chain variable region (CWH) (R98411) of 3H1, a murine monoclonal anti-idiotype antibody that mimics a specific epitope of the 180,000 mol.wt.

CC carcinoembryonic antigen (CEA) and which elicits an immune response in patients with advanced CEA-associated disease, e.g. colorectal cancer. It was obtd. by PCR amplification of 3H1 hybridoma DNA (see also T31545-46). The isolated polynucleotide, and/or a polynucleotide (see also T31540) coding for the VL region (R98410) of 3H1 can be used to design probes and primers, in expression systems, and in pharmaceutical applns, including vaccines, gene therapy and genetic immunisation, partic. against cancer.
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Best Local S
Matches 31
                                                                                                                                   Anti-idiotype antibody 3H1 heavy chain variable region Anti-idiotype antibody 3H1; carcinoembryonic antigen; C tumour-specific antigen; tumour; colorectal cancer; lun adenocarcinoma; therapy; ss.

Mus musculus.
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T99435 stand
T99435;
27-APR-1998
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28-DEC-1995;
28-DEC-1994;
WO9738725-A1.
23-OCT-1997.
11-APR-1997; U05953
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WPI; 96-321850/32.
P-PSDB; R98411.
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l Similarity 90.08;
316; Conservative
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Pred. No. 1.13e-167;
0; Mismatches 32;
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Best Local (
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               04-JUL-1996.
28-DEC-1995; U17105.
28-DEC-1994; US-365484.
(KENT ) UNIV KENTUCKY.
Chatterjee M, Chatterjee S
WPI; 96-321809/32.
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12-APR-1996; US-631085.
(KENT) UNIV KENTUCKY.
Chatterjee M, Chatterjee S
WPI; 97-526218/48.
                                                                                                                                                                                                                                                                                                            11-OCT-1996 (first entry)
Monoclonal anti-idictype antibody 3H1 VH cDNA.
Anti-idictype antibody; monoclonal antibody; CEA;
carcinoembryonic antigen; tumour-associated antigen;
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Key
cds
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Q65630;
Q1-FEB-1995
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03-NOV-1993;
(IDEC-) IDEC
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A cDNA clone (T34542) codes for the heavy chain variable region (R99687) of monoclonal anti-idiotype antibody 3H1 (ATCC HB 1200 It was obtd. by PCR amplification (see also T34543-44) of cDNA derived from 3H1 hybridoma cells. Anti-idiotype antibody 3H1 elicits a specific immune response to a unique epitope of carcinoembryonic antigen (CEA) that is not present on other members of the CEA family or on normal adult tissues. 3H1 can be used as a vaccine to elicit immune responses in patients
                                                                                                      Treating B cell lymphoma with chimeric antibody causing rapid depletion of peripheral B cells, a antibodies and hybridomas Disclosure; Fig 4; 101pp; English.

The sequence is the murine variable region light murine anti-CD20 monoclonal antibody 2BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (first entry)
Murine variable region light chain from 2BS.
B cell lymphoma chimeric antibody; CD20; per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with advanced CEA-associated disease or, when labeled, tumour detection in imaging.
Sequence 462 BP; 106 A; 124 C; 117 G; 119
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
WO9411026-A.
                                                               Sequence
                                                                                    See also
                                                                                                                                                                                                                                        P-PSBD; R55214.
                                                                                                                                                                                                                                                                                                        Anderson DR,
                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-1994.
12-NOV-1993;
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384 BP;
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larity 90.0%;
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                                                                                                                                                                                                                                                                                                           Hanna
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37.2%;
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                                                                                                                                                                                                                                                                                                           Leonard
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Pred. No. 1.13e-167;
Score 265;
Pred. No. !
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                                                               106
                                                                                                                                                                                                                                                                                                        JE,
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                                                                                                                                                                                                                                                                                                           Newman
; DB 11;
5.98e-167;
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                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09411026-A.
26-MAY-1994.
12-NOV-1993; U10953.
13-NOV-1993; US-978891.
03-NOV-1993; US-149099.
(IDEC-) IDEC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                      Treating B cell lymphoma with chimeric antibody - against CD20, causing rapid depletion of peripheral B cells, also new antibodies and hybridomas place of the sequence of the sequence shows a vector contg. TCAEB, a gene encoding a chimeric anti-CD20 anti-CD20 for treatment of B cell lymphomas. TCAEB contains 4 transcriptional cassettes, human Ig light and heavy chain constant regions, dihydrofolate reductase, neomycin phosphotransferase and murine variable regions. The vector can be used to produce antibodies which cause depletion of peripheral blood B cells, including those associated with lymphoma. They mediate complement-dependent lysis and lyse target cells by antibody-dependent cellular cytotoxicity.
       1176
                                                                                                    1116
                                                                                                                                                                                                      1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B cell lymphoma cell lysis; ss.
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Q65629;
Q1-FEB-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                              See also Q65629-35.
Sequence 9208 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson DR,
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ccctggatttatgccacatccaacctggcttctggagtccctgttcgcttcagtggcagt 1235
                                                                           gccagctgaagtgtaagttacatccactggttccagcagaagccaggatcctccccccaaa 1175
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                                                                                                                                               CCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATGACTTGCAGG
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TO Chimeric antibody; CD20; peripheral blood
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                                                                                                                                                                                                                                                                        37.1%;
93.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                              Α;
                                                                                                                                                                                                                                                                     Score 264;
Pred. No. 3
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                                                                                                                                                                                                                                                                     DB 11; 1
3.17e-166;
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                                                                                                                                                                                                                                                                                            Length
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RESULT PER SULT PER S
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S Example 7; Page 128; 150pp; English.

C This cDNA seguence encodes a mouse-human chimeric antibody

C light chain (W24532) in which the variable region is derived

CC from mouse anti-human factor IX monoclonal antibody BC2 cDNA (see

CC T79899) and human sequences from the immunoglobulin RF-TS3'CL

CC framework. It was obtained by PCR amplification (see T79897-98)

CC of BC2 cDNA and insertion of the PCR product into F9HZHC 1-3 cDNA

CC (see T77374). Claimed anti-Factor IX chimeric antibodies are

CC useful in the treatment of thrombosis.

CC useful in the treatment of thrombosis.
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Best Local S
Matches 28
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24-UUL-1997.

17-JAN-1997; U00759.

24-CCT-1996; US-029119.

R 17-JAN-1996; US-010108.

R 17-JAN-1996; US-010108.

GOMEK ) SMITHKLINE BEECHAM CORP.

A (SMIK ) SMITHKLINE BEECHAM CORP.

B (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

I Blackburn MN, Church WR, Feuerstein GZ, Gross MS;

I Nichols AJ, Padlan EA, Patel AH, Sylvester DR;

R WPI; 97-385117/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-Factor IX MAb chimeric light chain cDNA.
Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody; chimeric antibody; antibody engineering; light chain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T79900
T79900;
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Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W24532.
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tattactgccagtggagtattaacccacggacgttcggtggaggcaccaagctggaa
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No. 1.
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..68e-165;
.ches 18;
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TATTACTGCCAGCAGTGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAA 316

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                                                                                                                                                                                                                                                                                                                                                                                         This CDNA sequence encodes the light chain variable region (see W24520) of mouse anti-human Factor IX monoclonal antibody BC2. Claimed humanised antibodies (see W24510-18) contain CDRs (see W24504-09) of BC2 heavy and light chains inserted into framework regions of selected human antibody sequences. They have self-limiting neutralising activity, and are useful as anticoagulant agents in treatment of thrombosis associated with myocardial infarction, unstable angina, atrial fibrillation, stroke, renal damage, pulmonary embolism, deep vein thrombosis, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulation, sepsis, or artificial organs, shunts or prostheses (claimed). Also claimed are chimeric antibodies (see T79900), and Fab and F(ab')2 fragments. The claimed antibodies do not cause uncontrolled bleeding (contrast heparin and warfarin) since they sequence 321 BP; 78 A; 92 C; 79 G; 72 T;
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 28
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T77377 standard; cDNA; 321
T77377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-1997 (first entry)
Mouse anti-human Factor IX antibody BC2 light chain cDNA.
Monds anti-human Factor IX; anticoagulant; monoclonal antibody; antibody engineering; light chain; CDR;
humanised antibody; antibody engineering; light chain; CDR;
complementarity determining region; myocardial infarction;
angina; atrial fibrillation; stroke; kidney damage;
pulmonary embolism; deep vein thrombosis; coronary angiopla:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibition Example 5; Page 64; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
Blackburn MN, Church WR, Feuerstein GZ, Gross
Nichols AJ, Padlan EA, Patel AH, Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9726010-A1.
24-JUL-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nichols AJ, Padlar WPI; 97-385117/35.
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24-CCT-1996; US-029119.
17-JAN-1996; US-010108.
(SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shunt; prosthesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disseminated intravascular coagulation; artificial organ; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial
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                                                                                                        tattactgccagcagtggagtattaacccacggacgttcggtggaggcaccaagctggaa
                                 gggtctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgccact 252
                                                                                                                                                                                               gccagctcaagtgtaaattacatgcactggtaccagcagaagccaggatcctcccccaaa 132
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                                                                                                                                                                              GCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAA
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93.5%;
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Pred. No. 1.68e-165;
1; Mismatches 18;
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 312
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QY 257 TATTACTGCCAGCAGTGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGTCCAAGCTGGAA 316
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Db 313 atcaaa 318 || || ||

Qy 317 ATAAAA 322

Search completed: Sat Jan 9 12:38:18 1999 Job time : 122 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (C) 1993-1998 University of Edinburgh, U.K.	
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Sat Jan 9 11:32:13 1999; MasPar time 954.49 Seconds 1335.831 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: >US-08-704-178-1 (1-712) from US08704178.seq (1 of 712 1 ATGGACCTGCAGCTGACCCA......GGACCACGGTCACCGTCTCC 712
TACCTGGACGTCGACTGGGT......CCTGGTGCCAGTGGCAGAGG 4

Scoring table: TABLE default Gap 6

Nmatch

STD :

Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: embl-est55

1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
genbank-est107
5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est20
18:gb_est21 19:gb_est3 20:gb_est4 21:gb_est5 22:gb_est6
23:gb_est7 24:gb_est3 25:gb_est9 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

Statistics: Mean 10.709; Variance 1.855; scale 5.772

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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11 12 13	10	4001	321	Result
81 80	888	146 110 92 86	232 179 160	Score
11.4 11.4 11.2	11.9 11.5	20.5 15.4 12.9	32.6 25.1 22.5	Query Match
		345 335		Length DB
16 24	24 16	15 9 11 24	111	BG
T28938 H25625 AA300732	AA300571 AA291381 T27593	AI007196 AA569186 AA710291 AA318377	AA691311 AA592800 AI180569	ID
EST61186 Homo sapiens y148g05.rl Homo sapien EST13847 Testis tumor	EST13661 Testis tumor zt44g02.rl Soares ovar EST100653 Homo sapiens	ua73g04.rl Soares 2NbM nm30d10.sl NCI_CGAP_Li vt53a04.rl Barstead mo EST20620 Spleen I Homo	vs14f01.rl Barstead mo vo25g11.rl Barstead mo uc70f09.rl Soares mous	Description
4.51e-118 4.51e-118 6.81e-116	7.88e-127 2.95e-120 2.95e-120	1.74e-265 1.05e-182 2.72e-142 4.99e-129	0.00e+00 0.00e+00 0.00e+00 3.63e-298	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
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hll.rl Homo sap	ST100987 Pancreas tu	x78cl2.rl Soare	-	89603 Small intest	STS	0a03.rl Soares m	3g01.s1 NCI_CGA	v38g06.rl Soare	165d05.rl Homo sap	122f09.rl Homo	Homo s	e01.rl Barstead	cl Homo sa	20808 Splee	4 Homo sap	rl Soares c	' Esophagus).rl Homo sap	Lr1 Hc	14181 Testis tu	3h09.r1	Oc10.r1 Barstea	.rl Soa)5 Gall bladd	71 Pancreas t	3.rl Homo sap	ST100400 Pancrea	.01165 Thymus	54b07.r1 Str	e08.rl	EST142/9 Test1s tumor
	. 29e-	. 29e-	.29e-	.29e-	.29e-	.65e-	- 1	.32e-	.26e-	.26e-	.26e-	.26e-	.42e-	.78e-	.78e-	.32e-	.32e-	.62e-	.65e-	.65e-	. 23e-	.23e-	. 23e-	.22e-	.22e-	.22e-	.51e-	.02e-	.02e-	.02e-	. BIE-

ALIGNMENTS

FEATURES SOUTCE		TITLE JOURNAL COMMENT	REFERENCE AUTHORS	NID KEYWORDS SOURCE ORGANISM	RESULT 1 LOCUS DEFINITION
Seq primer: -28m13 rev2 ET from Amersham. Location/Qualifiers 1. 396 /organism="Mus musculus" /strain="FVB/N" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified	Contact: Marra M./Mouse EST project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	Geisel.S., Kucaba.T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. The WashU-HHMI Mouse EST Project Unpublished (1996)	<pre>Bukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 396) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,</pre>	AA091311 9269247 EST. house mouse. Mus musculus	AA691311 396 bp mRNA EST 16-DEC-1997 vs14f01.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone 1138201 5' similar to gb:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.

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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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Matches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA592800 344 bp mRNA EST 17-SEP-1997 vo25g11.rl Barstead mouse irradiated colon MPLRB7 Mus musculus clone 1050980 5' similar to gb:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence. AA592800
                                                                                                                                                                                                                                                                                                                                                                                                                                           g2406463
EST.
Fax: 314 400 1117 Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL;
This clone is available royalty free through LLNL;
                                                                                                                                                                                                                                                         Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 344)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                      The WashU-HHMI Mouse Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                               Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
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llarity 89.6%;
Conservative
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Pred. No. 0.00e+00;
1; Mismatches 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 CTCACTCAATCTCCAGCAATCATGTCTGCTTCTCCAGAGGGAGCAATGTCACCACGACCT 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTG
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                                                                                                                                                                                                                                                                                                 AI180569 310 bp mRNA
AI180569 10 mRNA
COOTO199.1 Soares mouse mammary gland NbMG Mus musculus cDNA clone
1431017 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION
(HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene
                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata;
Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226;
                                                    Marra,M., Hillier,L., Allen,M., Bowles,M., Districh,N., Dubuque,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Unpublished (1996)
                                                                                                                                                                                                                                                g3731207
                                                                                                                                                                                                                                                                  AI180569
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Location/Qualifiers
                       The
                                                                                                                                                                                                           house mouse.
                     WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                 complete (MOUSE);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 3']; double-stranded CDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. "/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Barstead mouse irradiated colon /dev_stage="8 weeks" /lab_host="DH10B" <1. >344
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/strain="FVB/N"
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91 c
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Pred. No. 0.00e+00;
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                                                                                                                                                                     Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                               CAAAAGTTCAAGGGCAAGGCAGCATTGACTGTAGACACATCCTCCAGCACAGCCTACATG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
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                                                          g3216753
EST.
                                                                                                (MOUSE);,
AI007196
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Washin-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                 AI007196 294 bp mRNA EST 12-JUN-1998 ua73g04.rl Soares 2NbMT Mus musculus cDNA clone 1363158 5' similar to gb.M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb.M12376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMAGE Consortium (info@image.llnl.gov) for MGI:915085
                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                     house mouse
                                                                                                                               Mouse immunoglobulin H-chain V-region pseudogene mRNA, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="mammary g
/tissue_type="mammary g
/dev_stage="4 weeks"
/lab_host="DH10B"
a 77 c 85 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
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/clone="1431017"
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/strain="C57BL/6J"
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79.3%;
                                                                                                               sequence
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Pred. No. 3.63e-298;
0; Mismatches 58;
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further information.
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                                                               TGCAGCTCAGCAGACTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAG
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                                                                                                          CCAGAAGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACA-
                                                                                                                                        TCAAAAGTTCAAGGACAAGGCCACATTGACTGTAGACAAATTCACCAGCACAGCCTACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. La
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1 (bases 1 to 294)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub.
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality Seq primer: -28ml3 rev2 ET from Amers High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston,R.
The WashU-HHMI Mouse EST Project
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/dév_stage="4 weeks"
/lab_host="DH10B"
a 68 c 77 g
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/clone="1363158"
                                                                                                                                                                                                                                                                                                                                                                                 20.5%;
                                                                                                                                                                                                                                                                                                                                                                  Score 146; DB 15;
Pred. No. 1.74e-265;
0; Mismatches 66;
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 294;
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                     338 GAGCTTAGCAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGTGCGAG 387
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 GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
                                                                                                                                                                                                                                                  TGTAAGGCATCTGGATTCACCCTCACCAACTGCCATATGCACTGGGTGCGACAGGCCCCT 217
                                                                                                                                                                                                                                                                                                                       GTCCAACTGGTGCAGTCTGGGGCTGAGGTGAAGAGCCTGGGGCCTCAGTGAAGCTTTCC 157
                                                                                                              CAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTATATG 337
                                                                                                                                                                                                                                                                                                    GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCC 424
                                                                                                                                                 GGGCAAGGGCTTGAGTGGGTGGGAATGATCAATTCTAGTGATGGTTATATAAGTAACGCA 277
                                                                                                                                                                                                                          TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA569186 387 bp nnm30d10.s1 NCI_CGAP_Lip2 similar to gb:L02325 IG H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing C Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia;
Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 387)
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AA569186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
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h quality sequence stop: 284.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1061683"
/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH10B"
<1...>387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/note="Vector: pAMF10; mRNA made from liposarcoma, cDNA made by oligo-dr priming. Non- directionally cloned.
Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56:5380-5383
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95 c
                                                                                                                                                                                                                                                                                                                                                                                             Score 110; DB 9; L
Pred. No. 1.05e-182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA EST
2 Homo sapiens cDNA clone I
HEAVY CHAIN PRECURSOR V-I
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                         Query Match 12.9%;
Best Local Similarity 66.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
  132
                                                                                                                                                                   14
                     CTAGAGCACTGATTTACTCGGCATCCTACCGGTACAGTGGAGTCCCTGATCGCTTCACAG
                                                                                                                                                                   TGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATGACTTGC
CCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTG
                                                                                                      AAGCCAGTCAGAATGTGGGTACTAATGTAGCCTGGTATCAAGAGAAACCAGGGCAATCTC
                                                                                                                                                                                                          TGACCCAGTCTCAAAAATTCATGTCCACATCAGCTGGAGACAGGGT-CAGCGTCACCTGC
                                                                                AGGGCCACCCCAA-GTGTA-AGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCC
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 345)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vt53a04.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone 1166766 5' similar to gb:x02484_rnal IG KAPPA CHAIN PRECURSOR V-IV REGION (HUMAN); gb:J00560 mouse ig kappa mrna from mopc21 6 other myeloma mrna 3' (MOUSE);, mRNA sequence.
AA710291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
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n quality sequence stop: 140.
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                                                                                                                                                                                                                                                     Conservative
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                          /dev_stage="8 weeks"
/lab_host="DH10B"
81 c 88 g
                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Barstead
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="1166766"
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                                                                                                                                                                                                                                                 Score 92; DB 11; LC
Pred. No. 2.72e-142;
""" wismatches 99;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G. L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGAGTATTTCTGTCAGCAATATAACAGCTTTCCGTACACGTTCGGAGGGGGGGACCAAGC 333
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AA318377
g1970863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056
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EST20620 Spleen I Homo
                                                                                                                                                                                                                                                                                                                                 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                    primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                            3018699423
                      87
                                                                                                                                                                                                                                                                                                                                                                                                                arkerlav@tigr.org
                                                <u>^</u>
                                                                                                                                       /note="Organ: spleen; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):119058"
/db_xref="taxon:9606"
                                                                  /dev_stage="adult, 23 yrs"
                                                                                         /sex="male"
                                                                                                                     /clone_lib="Spleen I"
                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Best Local Similarity 67.1%;
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 AGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAACCTTGGATTTATACC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 AGCTATTTACATTGGTATCAGCACAAACCAGGTAAAGCCCCCTAAACTCCTGATCTATGNT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Sprigs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Dimke, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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Contact: Kerlavage, AR
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                                                                                                                                Email: arkerlav@tigr.org
For clone availability, additional sequence and ex
information related to this EST, please check the
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                            Tel: 3018699056
                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                        Bioinformatics
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                                                                                                       primer: M13 Reverse
/note="Organ: testis;
                            /organism="Homo sapiens"
                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (6547 Suppl),
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Pred. No. 4.99e-129;
1; Mismatches 77;
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similar to similar
(GB:M18512), mRNA
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he TIGR Human
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Vector: pBluescript SK-; Site_1:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21449(2.r1 Soares ovary tumor NbHOT Homo sapiens 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                               Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. washU-Merck EST Project Unpublished (1995)
                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1576 Std Error: 0.00 Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 361.
                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                       Hillier,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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larity 72.3%;
Conservative
                                                                                                                                                                                                                                         est@watson.wustl.edu
EcoRI; Site_2: XhoI"
/db_xref="AfCC (inhost):192212"
/db_xref="taxon:9606"
/clone_lib="Testis tumor"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      545 CAGAAGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATG
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mes 191; Conser
RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehn, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,
Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Melssner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of CDNA Sequence
Other_ESTs: THC24356
Contact: Venter, JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGAGTTTTCAGGACAGAGTCAGCTTGACCACTGACACATCCACGAATACAGCCTACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T27593 393 bp mRNA EST 06-SEP-1995 EST100653 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region (GB:L01279) (HT:3043).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  light chain, T27593
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 393)
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llarity 65.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
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/clone="725234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archonta; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         393 bp
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No. 2.95e-120;
Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GACCTGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACAC 63
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S.,
Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Philips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
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Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGTCCAAGCTGGAAATAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTCACTTGCCGGGCAAGTCAGAGCATTAGCACCTTTTTAAATTGGTATCAGCAGAAACC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGGACCAAGGTGGAGGTCAAA 374
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932 Clopper Rd, Gaithersburg, MD 20
Tel: 3018699056
Fax: 3018699423
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T28938
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For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria;
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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                                                                                                                                                                                                                                                                                                                                                                                    theria; Archonta; Primates; Catarrhini;
(bases 1 to 209)
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65.9%;
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2.95e-120;
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                                                                                                                                                                                                                                                           double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7773 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares
                                                                                                                                                                                                                                                                                                                                    134;
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 2
Tel: 3018699056
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                                                 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lenon,G., Marra,J.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. an
                                                                                                                         Deuterostomia; Chordata; Vertebrata; Gnathostomata; Os
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
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                   The WashU-Merck EST
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Local Similarity 66.7%;
Nes 154; Conservation
                                                                  RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wal, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Pillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
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WashU-Werck EST Project
Washington University Schoo
4444 Forest Park Parkway, B
Tel: 314 286 1800
Fax: 314 286 1810
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 AGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTCGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 CATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 GCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCAC 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA301347
EST14279
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N. H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Barle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Sandek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA301347 413 bp mRNA EST 18-APR-1997 EST14279 Testis tumor Homo sapiens cDNA 5' end similar to simil to immunoglobulin kappa light chain, V region (GB:L01279), mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other_ESTs: THC87411
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                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 3018699423
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                                                                                                                                                                                                                                                                                      (bases 1 to 413)
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/note="Organ: testis; Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
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/db_xref="ATCC (inhost):192041"
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Pred. No. 6.81e-116;
Pred. No. 6.81e-106;
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Best Local Similarity 65.9%;
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AII16236 116 bp mRNA uc18e08.rl Soares mouse mammary gl 1398374 5' similar to gb:M87789 IC gb:X67210 M.musculus rearranged in (MOUSE); mRNA sequence.
AII16236 g3516560
                                                                                                                                                                                                                      AGGGAAAGCCCCTAAGCTCCTGATGTATGGTGCATCCAGTTTGCAAGGTGGGGTCCCTTC 256
                                                                                                                                                                                                                                                                                                                                TGAAGATTTTGCAACTTACTACTTTCAGCAGAGTTACAGTCCTCATCAGAAGGTTCGGCC 376
                                                                                                                                                                                                                                                                                                                                                                                          TCGCTTCAGTGGCGGTGGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGC 240
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96026280
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial assessment of human gene diversity and expression based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 3018699056
Fax: 3018699423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dimke,D.,
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ECORI; Site_2: XhoI"
//db_xref="ATCC (inhost):191658"
//db_xref="taxon:9606"
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Pred. No. 6.81e-116;
1; Mismatches 104;
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                                                                                     gland NbMMG Mus musculus cDNA clone IG GAMMA-1 CHAIN C REGION (HUMAN);
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                        AACTCAGCAGCCTGACATCTGAGGACACTGCGGTCTATTACTGTGGAAG 110
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AGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
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1 (bases 1 to 116)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST project
Washington University School of Medicinep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
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Seq primer: -28ml3 rev2 ET fro
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Fax: 314 286 1810
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larity 86.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
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(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
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/strain="C57BL/6J"
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/dev_stage="4 weeks"
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

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Title: Tabular output not generated. >US-08-704-178-1 (1-321) from US08704178.seq (2 of 4) 321

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 ATGGACCTGCAGCTGACCCA......GGGTCCAAGCTGGAAATAAA 321
TACCTGGACGTCGACTGGGT......CCCAGGTTCGACCTTTATTT

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 567134 seqs, 1101898692 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database:

Statistics:

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_v1 13:em_ro 14:em_v1 13:em_ro 14:em_v2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov 15:gb_ba1 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov 21:gb_pat 22:gb_ph 23:gb_pl1 24:gb_pl2 25:gb_pr1 26:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 30:gb_sts 31:gb_sy 32:gb_un 33:gb_vi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 9.835; Variance 4.583; scale 2.146

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179	CTGGAGTCCCTGC	CAACCIGGCII	AGGATCCTCCCCAAACCTTGGATTTATACCACATCCAACCTGGCTTCTGGAGTCCCTGC	CAAACCTTGG	GGATCCTCCCC	120 A	뫄
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                                                                                                                                                                                                                              Unknown.
Unknown.
                                                                                                                         A36642
Sequence
A36642
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T51657
        1 (bases 1 to 315)
Seemann,G. and Bosslet,K.
Antigranulocyte antibody of Patent: EP 0585570-A 2 09
                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 93.3%, 294; Conservative
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Seemann,G. and Bosslet,K.
Granulocyte-binding antibody constructs,
Patent: US 5645817-A 3 08-JUL-1997;
                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                               g2293945
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                                                   Murinae; Mus.
                                                                                           house mouse
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1. .315
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92 c 80 g
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93.3%;
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patent US 5645817.
(DE)
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Pred. No. 3.01e-209;
1; Mismatches 19;
          dy construct,
09-MAR-1994;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCAGTGGCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCATCAGAGTGGAAGCTGA
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Other
Other
Other
                                                                              Meek,K., Hasemann,C., Pollok,B., Alkan,S.S., Lucy, Urbain,J. and Capra,J.D.

Structural characterization of antiidiotypic antibodies.

Structural characterization the germline differently than
                                                               J. Exp. 1
89094248
                                                                                                                                                 Submitted (09-JAN-1989) K. Meek, Medical School, 5323 Harry Hines
                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; I
                                                                                                                                                                                                                                    Mus musculus
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Ig kappa light chain;
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X58586 Y00794
                                                                                                                                                                                                                                                                                                  Mouse hybridoma
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                                                                                                                                                                                  Meek, K.
                                                                                                                                                                                                      Murinae; Mus
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Similarity 93.3%;
                                                                                                                                        75235, USA
                                                                                                                                                                                                                                                 house mouse.
                                                                                                                              (bases 1 to 321)
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                                                                        Ab2s are derived from the germline xp. Med. 169 (2), 519-533 (1989)
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/db_xref="taxon:10090"
/cell_type="hybridoma/myeloma"
/2 c 80 g 71 t
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1. .315
          /organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
                                                   Location/Qualifiers
/cell_line="Hybridoma 2D3-K"
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Pred. No. 3.01e-209;
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                                                                                                                                                University of Texas Blud. Microbiology,
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Myomorpha;
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                                                                                                                                                            Southwestern
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RESULT 6
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Best Local Similarity
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                                                                                                                                                                                                                                                                      Mus sp.
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entry [NCBI gibbsq 118382] from the original journal article. This sequence comes from Fig. 5.
Location/Qualifiers
                                                                                                      Linnenbach, A.J.

Molecular cloning of murine monoclonal anti-idiotypic
J. Immunol. Methods 155 (1), 77-89 (1992)
                                                                                                                                                                                                                                Eukaryotae;
Vertebrata;
                                                                                            93017981
                                                                                                                                                                 1 (bases 1 to 312)
Kasai, Y., Herlyn, D.,
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larity 94.8%;
Conservative
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/db_xref="pID:g938245"
/translation="QIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPK
PWISATSNLASGVPARESGSGSGTSYSLTISRVEAEDAATYYCHQWSSNPPTFGGGTK
LEIKR"
92 c 80 g 71 t
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/note="variable region"
/product="IG kappa light chain"
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/note="variable region"
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/note="variable region"
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Eutheria; Rodentia; Sciurognathi; I
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Pred. No. 3.01e-209;
1; Mismatches 14;
                                                                                                                                                                   Sperlagh, M.,
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, 312 nt].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGGCCAGCTCAAGTGTAAGTTACATGCACTGGTACCAGCAGAAGCCAGGATCCTCCCCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGT-CACAATGACTTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                            ACTTATTACTGCCAGCAGTGGAGTAGTAACCCATGGACGTTCGGTGGAGGCACCAAGCTG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTTATTACTGCCAGCAGTGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGTCCAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATGACTTGC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCC 133
                                                                                                                                                                                                                                                        Mus musculus partial cds. AF056217
                                                          2 (bases 1 to 318)
Sandstrom,P., Johansson,A., Ullen,A.,
Direct Submission
                                                                                                                          Sandstrom,P., Johansson,A., Ullen,A., Behravan,G. and Stigbrand,T. Differences in sequence and affinity between three monoclonal anti-idiotypic antibodies against one anti-placental alkaline
                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 318)
Sandstrom,P., Johansson,A., Ullen,A., Behravan,G. an
                                       Sweden
                                                Submitted (30-MAR-1998) Immunology,
                                                                                                   Unpublished
                                                                                                                phosphatase idiotypic antibody
                                                                                                                                                                                                                                            g3044131
                                                                                                                                                                                                                                                                                             AF056217
                                                                                                                                                                                                                    house mouse.
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                         Location/Qualifiers
/organism="Mus musculus"
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/translation="VMTQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPKPW
TYATSNLASGVPARESGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPWTFGGGTKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /partial
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/db_xref="taxon:10095"
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/note="anti-idiotypic Fab;
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/gene="Ig V<down>&kgr;</down>"
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                                                                                                                                                                                                                                                                              monoclonal antibody aH7:38 IgG1
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. No. 1.51e-206;
Mismatches 17;
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                                                  Umea
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                                                                          Behravan, G. and Stigbrand, T
                                                University,
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                                                  Umea 90185,
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Mouse Ig k
                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                              sequence
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Query Match 83.2%;
Best Local Similarity 92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCTCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCG
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                                                                                                                                                                                                                                                                                   1 (bases 1 to 1370)
Parslow,T.G., Blair,D.L., Murphy,W.J. and Granner,D.K.
Structure of the 5' ends of immunoglobulin genes: A no
                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin-kappa.
Mouse 70Z/3 cell DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g196460
C-region; V-region; immunoglobulin light chain;
                                                                                                                                                                           Corrections to the sequence were sent
Dr. Tristram G. Parslow on Dec. 9, 199
                                                                                                                                                                                                                                                                                                                                                           Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAAR 1370 bp DNA
Ig kappa active V-region
                                                                                                                                                                                                                                            Natl. Acad. Sci. U.S.A. 81, 2650-2654 (1984)
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/number=1
join(776.
                                         /organism="Mus musculus"
/db_xref="taxon:10090"
<776. .824
/note="Ig kappa chain va
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/db_xref="PID:g3044132"
/translation="DIQLTQSPAILSASPGEKVSMTCRASSSVSYIHWYQQKPGSSPK
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/cell_line-"hybridoma"
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alkaline phosphatase antibody; variable region"
                                                                                                                                                        Location/Qualifiers
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                                       kappa chain variable region"
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Pred. No. 1.51e-206;
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                                                                                                                                                                           ent by Dr.
1991.
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                                                                                                             Lohman, K.L., Kieber-Emmons, T. and Kennedy, R.C. Molecular characterization and structural modeling of immunoglobulin variable regions from murine monoclonal specific for hepatitis B virus surface antigen Mol. Immunol. 30 (14), 1295-1306 (1993)
                                                                                                                                                                                                                                                                                                                    immunoglobulin light chain;
variable region.
                                                                                                   94019421
                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; N
                                                                                                                                                                                                                                                                 Mus musculus
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1003. >1337
/note="Ig kappa chain variable re/number=2
1338. >1369
/note="kappa cds intron J-C"
a 273 c 253 g 440 t
               /organism="Mus musculus"
/db_xref="taxon:10090"
101 c 89 g 7
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CRASSSVSYMHWYQQKPGSSPKPWIYATSNLASGVPARFSGSGSGTSYSLTISRVEAE
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/db_xref="PID:g196461"
                                                                              Location/Qualifiers
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94.1%;
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Myomorpha;
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Best Local
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Best Local Similarity
Matches 282; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 CAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 CAAACCCTGGATTTATGCCACATCCAACCTGGCGTCTGGAGTCCCTGCTCGCTTCAGTGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 CAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 CAGGGCCAGTTCAAGTGTAGGTTCCATACACTGGTACCAGCAGAAGCCAGGATCCTCCCC 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Hellstroem, I. and Hellstroem, K.E.
Production of a mouse-human chimeric monoclonal antibody to with potent Fc-dependent biologic activity
J. Immunol. 139, 3521-3526 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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C-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa; processed gene.
Mus musculus cDNA to mRNA.
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M17954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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iu, 02-FEB-1987.
   Conservative
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                                                                                  /note="V-region end/J-5-region /organism="Mus musculus" 112 c 93 g 98 t
                                                                                                                                                                       /product="immunoglobulin kappa-chain"
/db_xxef="PID:g466303"
/translation="kubryOQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMT
/translation="kubryOKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAE
                                                                                                                                         DAATYYCQQWSFNPPTFGAGTKLELK" 370. .371
                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/cell_line="2H7"
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                                                                                                                                                                                                                                                          note="V-J-5 region"
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                  81.6%;
94.3%;
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Score 262; DB 28;
Pred. No. 4.70e-202;
1; Mismatches 15;
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Pred. No. 9.46e-205;
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Local Similarity 94.3%;
hes 282; Conservative
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       Ig V kappa =anti-sigma receptor
cell line 10G9, mRNA Partial, 47
S76823
g913971
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109200
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                                                                                                                                                                                                                                                                                                                                                                              Unclassified.

1 (bases 1 to 403)
Robinson, R.R., Liu,
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113 c 92 g
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from 1
                                           477 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent WO 8900999.
                                                                                                                                                                                                                                                                  Score 262; DB 21; L
Pred. No. 4.70e-202;
1; Mismatches 15;
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Best Local :
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                                                                                                                                                                  430 ATAAA 434
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                                                                                                                                                                                                                             TATTACTGCCAGCAGTGGAGTCGTAACCTGTACACGTTCGGCGGGGGGGACCAAGCTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                          GCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAA
                                                        127490
Sequence
127490
                                          g1818266
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| Similarity 93.4%;
| 285; Conservative
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Mus sp.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
Unknown
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Molecular cloning of cDNAs for immunoglobulin variable regions
monoclonal anti-idiotypic antibody specific for sigma receptors
J. Neuroimmunol. 57 (1-2), 129-135 (1995)
                 Unknown
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CRASSSVSYIHWYQQKPGSSPKPWILATSNLASGVPARFSGSGSGTSYSLTISRMEAE
DAATYYCQQWSRNLYTFGGGTKLEIKRLMLHQLYPSSHHP"
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sigma receptors; This sequence comes from Fig. 4"
/codon_start=1
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/db_xref="PID:g913972"
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/gene="Ig V&kgr;"
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/db_xref="taxon:10095"
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I05923
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Chimeric antibody with specificity to Patent: EP 0274394-A2 39 13-JUL-1988;
Location/Qualifiers
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Hoogenboom, H.R.J.M., Baier, M., Jespers, L.S.A.T. and Winter, G.P. Production of chimeric antibodies - a combinatorial approach Patent: US 5565332-A 4 15-OCT-1996;
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Pred. No. 2.95e-200;
1; Mismatches 16;
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Pred. No. 3.72e-201;
1; Mismatches 25;
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87304452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; I
Murinae; Mus.
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house mouse.
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                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
/cell_type="hybridoma"
1..309
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91 c 76 g 71
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Pred. No. 1.84e-198;
1; Mismatches 17;
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mRNA (NQ18.36.44L)
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MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Sat Jan 9 14:31:15 1999; MasPar time 60.25 Seconds 724.916 Million cell updates/sec

Description: Perfect Score: N.A. Sequence: Title: >US-08-704-178-1 (1-321) from US08704178.seq (2 of 4) 321

Comp: 1 ATGGACCTGCAGCTGACCCA......GGGTCCAAGCTGGAAATAAA 321
TACCTGGACGTCGACTGGGT......CCCAGGTTCGACCTTTATTT

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0 188442 segs, 68026449 bases

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Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

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8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 8.055; Variance 4.678; scale 1.722

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Score	Query	Query Match Length DB	DB	ID	Description	Pred. No.
ב	314	97.8	711	ٔ و	Q55180	Sequence encoding the	2.02e-204
2	314	97.8	711	29	T65006		2.02e-204
ω	312	97.2	711	18	T17728	Anti-erbB2 scFv cDNA.	5.83e-203
4	264	82.2		11	Q65630	Murine variable regio	
ري ري	262	81.6		34	T79900	Anti-Factor IX MAb ch	
o	262	81.6		34	T77377	Mouse anti-human Fact	
7	262	81.6	335	34	T79899	Anti-Factor IX MAD BC	
œ	262	81.6		2	N70972	2H7 VL sequence in wh	
9	262	81.6		\vdash	N91147	2H7 Vh sequence.	
10	262	81.6		30	T51043	Coding sequence for 1	1.52e-166
11	262	81.6		32	T36317	2H7 antibody light ch	1.52e-166
12	262	81.6		31	T70869	2H7 light chain varia	1.52e-166
13	262	81.6	426	40	V03927	Mouse 2H7 antibody li	1.52e-166

Query Match 97.8%; Best Local Similarity 99.7%; Matches 320; Conservative

Score 314; DB 9; Le Pred. No. 2.02e-204; 0; Mismatches 0;

Length 711; Indels

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3.91e-149 3.91e-149	.91e-14 .91e-14	.91e-14	.37e-15	.39e-15	.39e-15	.39e-15	.62e-15	.62e-15	.75e-15	.75e-15	.30e-15	.22e-15	.47e-15	47e-15	./6e-15	.76e-15	.77e-16	.45e-16	.49e-16	.07e-16	.52e-16	.52e-16	.52e-16

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                                                                                                 The present cDNA sequence codes for a claimed single-chain antibody, codesignated e23(FV), which binds to erbB-2. Monoclonal antibody e23 was generated by immunising mice with NyerbB-2 cells overexpressing the 9pl85 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light- chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide in the resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbB-2 gp185 marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours. So Sequence 711 BP; 175 A; 182 C; 189 G; 164 T;
                                               Query Ma
Best Loc
Matches
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24-DEC-1996.
07-OCT-1991; 772270.
07-OCT-1991; US-772270.
30-UUN-1992; US-906555.
11-MAY-1993; US-061092.
""" ARONEX PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                         (ARON-) ARONEX PHARM IN
Bird RE, Kasprzyk PG,
WPI; 97-064831/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single-chain anti-erbB2 antibody e23(Fv) cDNA.
Single chain antibody; variable region; light chain; heavy chain; breast cancer; ovarian cancer; non-small cell lung carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T65006 standard;
                                                                                                                                                                                                                                                                                                  cells expressing this protein Example 8; Columns 25-28; 28pp;
                                                                                                                                                                                                                                                                                                                               Single chain antibodies specific for erbB-2 protein, gp185 - wit labels or cytotoxin, useful for detection and treatment of tumour
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05-JUN-1997
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320; Conser
                                              97.8%;
larity 99.7%;
Conservative
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anti-erbB2 an
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1..711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 31
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06-SEP-1994; US-301339.
06-JUN-1995; US-468252.
06-JUN-1995; US-468252.
(UABR-) UAB RES FOUND.
Curiel DT, Deshane J;
WPI: 96-171307/17.
P-PSDB; R94020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 42; Page 29-30; 48pp; English.

A nucleac acid comprises a first sequence encoding a signal peptide (R94019) linked to a second sequence (T17728) encoding a single chain Fv fragment (R94020) that binds a human erbB2 oncoprotein.

The anti-erbB2 sFv portion is obtained by PCR using e23scFv plasmid as template. The signal peptide directs the scFv to the endoplasmic reticulum. The nucleic acid is incorporated into a plasmid or viral vector to facilitate expression of the scFv antibody homologue within e.g. an epithelial carcinoma cell. Intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 3
T17728
T17728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibition of proliferation or survival of, esp. malignant cells - by introducing nucleic acid mol. encoding antibody which is expressed and binds, pref. erbB2, protein intracel
                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression of the homologue inhibits surface expression of erbB2 and thereby inhibits cell proliferation and cell survival and decreases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-erbB2 scFv cDNA. Oncoprotein; erbB2; c
                                                                                                                                                                                                                                                                                                                                                                                                       tumorigenicity.
Sequence 711
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gene therapy; ds.
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aggatcctcccccaaaccttggatttataccacatccaacctggcttctggagtccctgc
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homologue
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Best Local S
Matches 28
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12-NOV-1993; U10953.
13-NOV-1992; US-978891.
03-NOV-1993; US-149099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reffme
WPI; 9
  T79900 standard;
T79900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p-psBb; R55214.

Treating B cell lymphoma with chimeric antibody - agrasting rapid depletion of peripheral B cells, also antibodies and hybridomas bisclosure; Fig 4; 101pp; English.

The sequence is the murine variable region light chamurine anti-CD20 monoclonal antibody 2BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (first entry)
Murine variable region light chain
B cell lymphoma chimeric antibody;
cell lysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q65630;
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q65630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        See also Q65629-35.
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                                                                                                                                                                                                                                                       cccagtctccagcaatcctgtctgcatctccaggggagaaggt-cacaatgacttgcagg 138
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                                                                                                                                         383
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                    CDNA;
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                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 264; DB 11;
Pred. No. 5.34e-168;
1; Mismatches 17;
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Best Local S
Matches 28
T7737;

26-DEC-1997 (first entry)

Mouse anti-human Factor IX antibody BC2 light chain cDNA. Thrombosis; therapy; Factor IX; anticoagulant; monoclonal arhumanised antibody; antibody engineering; light chain; CDR; complementarity determining region; myocardial infarction; angina; attial fibrillation; stroke; kidney damage; pulmonary embolism; deep vein thrombosis; coronary angiople; sincomplemental intravascular coagulation; artificial organ; sincomplemental coagulation; sincomplemental coagulation; sincomplemental coagulation; sincomplemental coagulation; sincomplemental coagulation; sincomplemental coagulation; sincomplemental coagu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This cDNA sequence encodes a mouse-human chimeric antibody light chain (W24532) in which the variable region is derived from mouse anti-human factor IX monoclonal antibody BC2 cDNA (see T79899) and human sequences from the immunoglobulin RF-TS3 CL framework. It was obtained by PCR amplification (see T79897-98) of BC2 cDNA and insertion of the PCR product into F9HZHC 1-3 cDNA (see T77374). Claimed anti-Factor IX chimeric antibodies are useful in the treatment of thrombosis.

Sequence 318 BP; 79 A; 91 C; 78 G; 70 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric Mus musculus.
Chimeric Homo sapiens.
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-DEC-1997 (first entry)
Anti-Factor IX MAD chimeric light chain cDNA.
Thrombosis; therapy; Factor IX; anticoagulant; monocle chimeric antibody; antibody engineering; light chain;
                                                                                                                                                                                                                                  T77377 standard; cDNA; T77377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; W24532.
Inhibiting thrombosis with self-limiting antibody to factor - avoids uncontrolled bleeding by providing on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blackburn MN, Church WR, Feuers: Nichols AJ, Padlan EA, Patel AH, WPI; 97-385117/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP.
(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
Blackburn MN, Church WR, Feuerstein GZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-1996;
17-JAN-1996;
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17-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                            ATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTACTGCCAGCAGTGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Page 128; 150pp; English.
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US-010108.
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                                                                                                                                                                                                                                                          ВP
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Pred. No. 1.52e-166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 318;
                            angioplasty;
organ; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation
                                                                                                                                                        antibody;
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RESULT TO THE PN WEEP PD 22
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Example 5; Page 64; 150pp; English.

Wa4520) of mouse anti-human Factor IX monoclonal antibody BC2.

Claimed humanised antibodies (see W24510-18) contain CDRs (see

W24504-09) of BC2 heavy and light chains inserted into framework

regions of selected human antibody sequences. They have self-

limiting neutralising activity, and are useful as anticoagulant

agents in treatment of thrombosis associated with myocardial

dinfarction, unstable angina, atrial fibrillation, stroke, renal

claimed, pulmonary embolism, deep vein thrombosis, percutaneous

transluminal coronary angioplasty, disseminated intravascular

coagulation, sepsis, or artificial organs, shunts or prostheses

(claimed). Also claimed are chimeric antibodies (see T79900), and

Fab and F(ab')2 fragments. The claimed antibodies do not cause

uncontrolled bleeding (contrast heparin and warfarin) since they

provide only partial inhibition of coagulation.

Sequence 321 Bp; 78 A; 92 C; 79 G; 72 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.

w09726010-A1.
24-JUL-1997.
17-JAN-1997; U00759.
24-OCT-1996; US-029119.
24-OCT-1996; US-029119.
(SMIK) SMITHKLINE BEECHAM CORP.
(UVVE-) UNLY VERMONT & STATE AGRIC COLLEGE.
Blackburn MN, Church WR, Feuerstein GZ, GR:
Nichols AJ, Padlan EA, Patel AH, Sylvester |
WPI; 97-385117/35.
27-DEC-1997 (first entry)
Anti-Factor IX MAb BC2 light chain PCR product. Thrombosis; therapy; Factor IX; anticoagulant; n chimeric antibody; antibody engineering; light chimeric Mus musculus. Chimeric synthetic.
w09725010-A1.
                                                                                                        T79899 standard;
T79899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial
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                                                                                                                                                                                                                          ATAAA
                                                                                                                                                                                                  atcaa 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
285; Conser
                                                                                                                                                                         321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                     cDNA; 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.6%;
93.4%;
                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feuerstein GZ, Gı
tel AH, Sylvester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e 262; DB 34; I
. No. 1.52e-166;
Mismatches 18;
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er DR;
                                                    chain;
                                                                monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA sequence was obtained by PCR amplification (see T79897 and T79898) of the light chain variable region (see also T77377) of mouse anti-human factor IX monoclonal antibody BC2 cDNA. The amplification resulted in the addition of ScaI, NarI ends to the VL region. The PCR product was ligated into ScaI, NarI-digested F9HZHC 1-3 (see T77374) and digested with ScaI, NarI to produce a mouse-human chimeric light chain F9CHLC (see T79900, W24532). Claimed anti-Factor IX chimeric antibodies are useful in the treatment of thrombosis.

Sequence 335 BP; 80 A; 97 C; 85 G; 73 T;
                                                                                   cds
                                                                                                                                                                                                                                                                                                                                                                                 09-APR-1991 (first entry)
2H7 VL sequence in which t
Chimeric antibody; Anti-ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N70972
N70972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W24531.
Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial
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24-OCT-1996; US-029119.
24-OCT-1996; US-010108.
(SMIK ) SMITHKLINE BEECHAM CORP.
(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
Blackburn MN, Church WR, Feuerstein GZ, Gr
Nichols AJ, Padlan EA, Patel AH, Sylvester
MPI; 97-385117/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atcaa 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; cDNA; 403
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                                                                                                                                                                                                                                                                                                                                                                                 antibody; Anti-cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.6%;
llarity 93.4%;
Conservative
/*tag= c
/label=CDR1
166..210
/*tag= d
/label=FR2
211..231
                                                                                                                                                            /label=FR1
139..165
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67..138
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Pred. No. 1.52e-166;
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N91147 standa
AC N91147;
DT 06-JUL-1990 (fi.
DE 2H7 vh sequence.
KW Antibodies; pasr
OS Synthetic.
"H Key
cds
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Best Local S
Matches 28
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07-MAY-1987
27-OCT-1986; U02269.
01-NOV-1985; US-793980.
(ITGE-) INT GENETIC ENG INC.
(ROBI/) ROIBINSON R R.
ROBINSON RR, Liu AY, HOTWITZ A
WPI: 87-136004/19.
                                                                                                                                                                                                                                                                                                                                                                                                                             The patentors claim a chimeric antibody molecule comprising 2 light chains and 2 heavy chains, each comprising a constant human region and a variable non-human region. Coding sequences for the Ig chains are also claimed. The invention provides consensus sequences of light and heavy chain J regions useful in the design of oligonucleotides (UIGS) for use as primers or probes for cloning immunoglobulinlight or heavy chain mRNAs or genes. Depending on the nature of design of a particular UIG, it may be capable of hybridizing to all Ig mRNAs or genes containing a single specific J sequence. UIG denotes universal immunoglobulin gene. Sequence 403 BP; 100 A; 112 C; 93 G; 98 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific antigens.
Example; Fig 22; 126pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cds
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                                                                                                                                            257
                                                                                                                                                                 338
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                                                                                                                                        999tctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgccact
                                                                                                                                                                                                                                                   gccagctcaagtgtaagttacatgcactggtaccagcagaagccaggatcctcccccaaa
                                                                                                                                                                                         GGGTCTGGGACCTCTTACTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACT
                                                                                                                                                                                                                                      CCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGT
                                                                                                                                                                                                                                                                                    GCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                    282;
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                              passive
                                                                                                                                                                                                                                                                                                                                                                                 81.6%;
llarity 94.3%;
Conservative
                                                                    (first
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/label=CDR2
232..327
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/label=CDR3
355..403
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349..403
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328..354
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/label=JK5
           Location/Qualifiers 20..403
                                                                                             DNA;
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                                            immunisation;
                                                                     entry 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                 Score 262;
Pred. No. 1.
1; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                 re 262; DB 2; Le
d. No. 1.52e-166;
Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wall
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                                                                                                                                                                                                                                                                                                                                                                                                          Length
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of
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PR C 2.2.2 PR R C 
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Best Local
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25-JUL-1988; 02514.
24-JUL-1987; US-077528
(ITGE-) Int Genetic Er
Robinson RR, Liu AY, I
WEI; 89-061144/08.
P-PSDB; P94778.
US5576195-A.
19-NOV-1996.
01-NOV-1985.
21-OCT-1986.
24-UUL-1987.
11-JAN-1988.
29-WAR-1990.
08-DEC-1992.
22-FEB-1993.
09-DEC-1994.
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T51040; tandard; cDNA; 426 BP.
T51043;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody; Ig;
myeloma cell;
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Sequence 403 BP; 100 A; 112 C; 93 G; 98 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; 7pp; English Sequence, derived from M
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793980.

US-793980.

WO-U02269.

US-077528.

US-142039.

US-501092.

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US-987555.

US-020671.

US-357234.
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Pred. No. 1.52e-166;
1; Mismatches 15;
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PR Hetter M, Lei S, Robinson RR, Wilcox GL;

DR P-95DB; W10243/01.

DR P-95DB; W10243/01.

PT Improved prodn. of protein in Gram -ve bacteria using signal proved prodn. of protein of antibodies

PT the cytoplasm, esp. for prodn. of antibodies

PT the cytoplasm, esp. for prodn. of antibodies

PT the cytoplasm, esp. for prodn. of antibody. The 2H7 antibody recognises

CC region of the 2H7 mouse monoclonal antibody. The 2H7 antibody recognises

CC the human B-cell surface antigen Bp35, which plays a role in B-cell

CC with human B-cell antiben specificity, that was produced using the method of the invention. The method of the invention is for the production of a protein in a Gram-negative bacterium. The method improves on current techniques, by using a vector including DNA encoding the pectate lyase immunisation (Tay), particularly those with a human constant region, cc suitable for passive immunisation (without risk of serum sickness or canaphylaxis) or for in vivo/in vitro diagnosis and imaging. The Ig may also be used therapeutically, optionally coupled to toxins, etc.

CC anaphylaxis) or for in vivo/in vitro diagnosis and imaging. The Ig may calso be used therapeutically optionally coupled to toxins, etc.

CC anaphylaxis signal sequence means that the protein is exported from the cytoplasm and can be recovered from the culture medium or periplasm, in a critical sequence means that the protein is exported from the culture medium or periplasm, continued and these can now be changed to G, A or E

CC classes.
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Best Local S
Matches 28
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21-JAN-1997.
                                                                                        mat_peptide
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                                                                                                                                                                                                                                          therapy; variable
                                                                                                                                                                                                                                                                      Immunoglobulin G: IgG: light chain; recombinant production;
antibody; passive immunisation; serum sickness; anaphylactic shock;
immunoassay; imaging; reagent; complement mediated lysis;
                                                                                                                                                                                                                                                                                                                                  21-OCT-1997 (first entry)
2H7 antibody light chain vari
Immunoglobulin G; IgG; light
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                                                                                  /*tag= a
109..426
                                                                                                                                                 Location/Qualifiers 43..108
                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA;
                                                                                                                                                                                                                                             region;
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                                                                                                                                                                                                                                             SS.
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Pred. No. 1.52e-166;
1; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PT dicistronic transcription unit with pectate lyase signal sequences PS Example; Fig 22; 95pp; English.

CC The present sequence encodes the light chain variable region of CC the 2H7 antibody. The 2H7 cDNA was used in the preparation of CC molecule comprises 2 DNA sequences encoding an Ig fragment. The DNA CC molecule comprises 2 DNA sequences encoding a pectate lyase secretion signal sequences respectively linked to a DNA sequence cc encoding an Ig Fd molecule or Ig light chain, operably linked to a Single prokaryotic promoter so as to form a dicistronic transcription unit, provided that the Ig fragment can bind an antigen and is produced and secreted by an E. coli host cell when CC the nucleic acid molecule is expressed in the host cell when CC manifyen and independent encourage of the production of recombinant antibodies, which can be used for passive immunisation CC without negative immune reactions (e.g. serum sickness and anaphylactic shock), in labelled forms as immunoassay or imaging creagents, in complement mediated lysis and for therapeutic purposes when coupled to a toxin or other therapeutic agent.

So Sequence 426 BP; 100 A; 135 C; 93 G; 98 T;
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29-MAR-1990;
01-NOV-1985;
27-OCT-1986;
27-JUL-1987;
11-JAL-1988;
11-JAL-1988;
11-JAL-1989;
18-AUG-1994;
                                                                                                                                                                                                                                                T70869;
04-SEP-1997 (first entry
2H7 light chain variable
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Better M, Horwitz AH, Lei S, Liu AY, Robinson F
Well R, Wilcox GL;
WPI; 97-107579/10.
P-PSDB; W10589.

Nucleic acid encodinding immunoglobulin fragment -
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                                                                                                                                                                                                                                                                                                                                        standard;
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US-501092.

US-793980.

WO-U02269.

WO-U7528.

US-077528.

US-142039.

US-987555.
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llarity 94.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                           cDNA; 426
                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                      sequence.
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Pred. No. 1.52e-166;
1; Mismatches 15;
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Antibody engineering; heavy chain; light chain; chimaeric antibo passive immunisation; diagnosis; hybridoma; monoclonal antibody; 247; B-cell antigen; Bp35; ss.

chain; light chain; chimaeric antibody;

mat_peptide signal_peptide

/*tag= a 241..426

/*tag= b

Location/Qualifiers 43..240

misc_feature

342..375

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Best Local
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01-NOV-1985; US-793980.

01-NOV-1985; US-019390.

27-OCT-1986; WS-0102269.

24-JUL-1987; US-077528.

11-JAN-1988; US-142039.

29-MAR-1990; US-501092.

17-APR-1992; US-870404.

29-APR-1994; US-235225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secretable immunoglobulin heavy and light chain fragments - capabl of assembling into chimeric antibodies, useful for e.g. passive immunisation, diagnosis, etc immunisation, diagnosis, etc example 4; Fig 22; 96pp; English.

A cDNA clone (770869) codes for the light chain variable region (W16344) of the 2H7 mouse monoclonal antibody, which recognises human B-cell surface antigen Bp35. The sequence was isolated from a 2H7 cell line cDNA library by PCR amplification. The 2H7 heavy chain variable sequence (T60868) has also been isolated. The sequences have been used to construct a human-mouse chimaeric antibody with specificity for the human B-cell antigen. Sequence 426 BP; 100 A; 135 C; 93 G; 98 T;
                                                                                                                            01-JUN-1998 (first entry)
Mouse 2H7 antibody light chain variable region cDNA.
Mouse; murine; light chain; variable region;
immunoglobulin fragment production; Ig fragment production; of the production of the p
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08-APR-1997.
                   mat_peptide
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                                                                     sig_peptide
                                                                                                                  Mus sp.
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                                                                                                                                                                                                                                                                                   V03927 standard;
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97-225473/20.
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109..426
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/note= "Jk5 sequence
406. 420
/*tag= d
                                                                   Location/Qualifiers 43..108
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94.3%;
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Pred. No. 1.52e-166;
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surface antigen; ss.
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PS Example TY; Fig 22; 98pp; English.

CC The present sequence was used in the development of a novel method CC for the production of an immunoglobulin (1g) fragment capable of CC binding an antigen. The method comprises culturing an E. coli host CC that has been transformed with a nucleic acid molecule encoding the CC and secreted. The nucleic acid molecule comprises DNA sequences concoding the CC and secreted. The nucleic acid molecule comprises DNA sequences concoding at least the variable region of CC an Ig fd molecule; and (b) pectate lyase secretion signal sequence coperably linked to a DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) are operably linked CC transcription unit. The method is used to produce chimeric Fab CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised CC against human B-cell surface antigen. The invention provides a CC novel approach for producing genetically engineered antibodies of CC expression in genetically engineered argument DNA cloning and production of CC expression in genetically engineered organisms. The application of CC expression in genetically engineered organisms. The application of CC expression in stibodies, recombinant DNA cloning and production of CC expression in the efficient large scale production of human CC monoclonal antibodies. The invention also provides an effective solution for the efficient large scale production of human CC monoclonal antibodies. The invention also provides an solution to CC the problem of class switching antibody molecules.

Sequence 426 BP; 100 A; 135 C; 93 G; 98 T;
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Best Local
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11-JAN-1988;
08-DEC-1992;
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02-DEC-1997.
25-MAY-1995;
29-MAR-1990;
LT 14
V18558
V18558;
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25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Production of chimeric antibody fragments -
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Better M, Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; W41071
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                                                                     tattactgccagcagtggagttttaacccacccacgttcggtgctgggaccaagctgga
                                                                                                                                                                                                                                                                      GCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAA
                                                                                                                                                                                                                                                                                                                                   CCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACACAATGACTTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                  282;
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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US-501092.
US-793980.
WO-U02269.
WO-U7528.
US-142039.
US-98755.
US-299085.
US-450731.
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                                                                                                                                                                                                                                                                                                                                                                                              Score 262; DB 40;
Pred. No. 1.52e-166;
1; Mismatches 15;
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standard;

CDNA;

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                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                               PT DNA encoding secretable immunoglobulin fragments - comprising at PT DNA encoding secretable regions of light or heavy chains

Example IV, Fig 22; 98pp; English.

CC The present sequence was used in the development of a novel method CC for the production of an immunoglobulin (Ig) fragment capable of CC binding an antigen. The method comprises culturing an E. coli host that has been transformed with a nucleic acid molecule encoding the CC Ig fragment, under conditions so that the Ig fragment is produced CC encoding: (a) pectate lyase secretion signal sequence operably and secreted. The nucleic acid molecule comprises DNA sequence coperably dinked to a DNA sequence encoding at least the variable region of CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence operably linked to a DNA sequence encoding at least the variable region of CC as single prokaryotic promoter to form a dicistronic transcription unit. The method is used to produce chimeric Fab CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised against human B-cell surface antigen. The invention provides a cc expression in genetically engineered antibodies of CC expression in genetically engineered antibodies of CC expression in genetically engineered antibodies of CC chemical gene synthesis, recombinant DNA cloning and production of the efficient large scale production of human cc constitution for the efficient large scale production of human cc constitution of class switching antibody molecules.

Sequence 426 BP; 100 A; 135 C; 93 G; 98 T;
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Best Local
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Better M, Horwitz AH, Lei
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Mouse 2H7 ar
                                  137
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    301
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98-051492/05.
                            CCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTTCAGTGGCGGT 196
                                                                                                                                                     999tct999acctcttactctctcacaatcagcagagtggaggctgaagatgctgcact
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WO-U02269
US-142039
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US-501092.
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109..426
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Pred.
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                                                                                                                                                                                                               e 262; DB 40; I
. No. 1.52e-166;
Mismatches 15;
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Ig fragment production;
                                                                                                                                                                                                                                              Length 426;
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Production of lecombination in the development of a novel method CC The present sequence was used in the development of a novel method CC for the production of an immunoglobulin (Ig) fragment capable of CC binding an antigen. The method comprises culturing an E. coli host CC binding an antigen. The method comprises culturing an E. coli host CC binding an antigen. The method comprises bulturing an E. coli host CC in that has been transformed with a nucleic acid molecule encoding the CC Ig fragment, under conditions so that the Ig fragment is produced CC and secreted. The nucleic acid molecule comprises DNA sequences CC encoding: (a) pectate lyase secretion signal sequence operably CC inked to a DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) are operably linked to a DNA sequence encoding at least the variable CC to a single prokaryotic promoter to form a dicistronic CC transcription unit. The method is used to produce chameric Fab CC against human B-cell surface antigen. The invention provides a CC novel approach for producing genetically engineered antibodies of CC desired variable region specificity and constant region CC expression in genetically engineered organisms. The application of CC chemical gene synthesis, recombinant DNA cloning and production of chemical gene synthesis, recombinant DNA cloning and production of constant of or the efficient large scale production of human more cloned in thodoles. The invention also provides a solution to the combinant of class switching antibody molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-1988;
08-DEC-1992;
18-AUG-1994;
                                                                       the problem of class switching antibody molecules. Sequence 426 BP; 100 A; 135 C; 93 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-1990;
01-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse 2H7 antibody light chain variable region cDNA. Mouse; murine; light chain; variable region; infinity fragment production; Ig fragment production monoclonal antibody 2H7; human B-cell surface antigen; ss.
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05-JUN-1998
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 282; Conse
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US-793980.

WO-U02269

US-077528

US-142039

US-142039

US-299085

US-299085

US-450731

US-466203.
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               81.6%;
94.3%;
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Score 262; DB 40;
Pred. No. 1.52e-166;
1; Mismatches 15;
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В

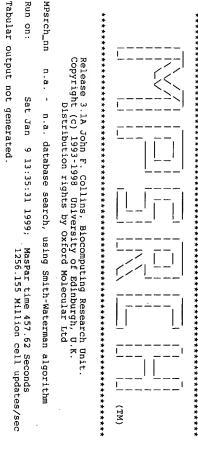
122 cccagtctccagcaatcctgtctgcatctccaggggagaaggt-cacaatgacttgcagg 180

Gaps

Search completed: Sat Jan 9 14:32:20 1999	Search
257 TATTACTGCCAGCAGTGGAGTCGTAGCCCACCCACCTTCGGAGGGGGGTCCAAGCTGGA 315	Qy 2
361 tattactgccagcagtggagttttaacccacccacgttcggtgctgggaccaagctgga 419	Db 3
197 GGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACT 256	Qy 1
301 gggtctgggacctctttactctctcacaatcagcagagtggaggctgaagatgctgccact 360	Db 3
137 CCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGCTTCAGTGGCGGT 196	Qy 1
241 ccctggatttatgccccatccaacctggcttctggagtccctgcttcgcttcagtggcagt 300	Db 2
77 GCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAA 136	Qy
181 gccagctcaagtgtaagttacatgcactggtaccagcagaagccaggatcctcccccaaa 240	Db 1
	Qy

Job time : 65 secs.

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		4.			



Title: >US-08-704-178-1 (1-321) from US08704178.seq (2 of 4) 321

Description:
Perfect Score:
N.A. Sequence:
Comp: Scoring table: 1 ATGGACCTGCAGCTGACCCA......GGGTCCAAGCTGGAAATAAA 321
TACCTGGACGTCGACTGGGT......CCCAGGTTCGACCTTTATTT

Nmatch STD Gap TABLE default Gap 6 Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases ×

Minimum Match 0% Listing first 45 summaries

Post-processing:

Database: embl-est55

1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
genbank-est107
5:gb_est1 6:gb_est107:gb_est11 8:gb_est129:gb_est13
10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est20
18:gb_est21 19:gb_est3 20:gb_est2 21:gb_est5 22:gb_est6
23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

Statistics: Mean 9.931; Variance 1.885; scale 5.267

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

13	10 11	870	4 D R	321	Result
77 76	79 78	79 79	8 8 8 2 1 4	232 179 91	Score
24.0	24.6	24.6	25. 25. 20.	72.3 55.8 28.3	Query Match
				396 344 345	Length DB
24 16	24	14	16	11 9 11	BB
AA295311 R69482	AA301347 AA295941 AA295093	AA921173 AA300732	AA318377 T27593	AA691311 AA592800 AA710291	ID
EST100471 Pancreas tum yj83c03.rl Homo sapien	EST14279 Testis tumor EST101165 Thymus III H EST100400 Dancross tum	y140903.ri Homo Sapien vy54b07.rl Stratagene EST13847 Testis tumor	EST20620 Spleen I Homo EST100653 Homo sapiens	vs14f01.rl Barstead mo vo25g11.rl Barstead mo vt53a04.rl Barstead mo	Description
4.67e-103 4.64e-101	4.61e-107 4.66e-105	4.53e-109 4.61e-107 4.61e-107	3.89e-117 4.41e-111	0.00e+00 0.00e+00 2.27e-131	Pred. No.

42 8A4/9857 42 8A6/9857 43 8A863906 vq50cl0.rl Barstead by 25 24 8A301261 EST14181 Testis tumor 52 24 8A301261 EST14181 Testis tumor 63 16 869532 yu40h01.rl Homo sapise 70 19 H62115 yu40h01.rl Homo sapise 8A405415 EST20808 Spleen I Homo sapise 8A405415 EST20808 Spleen I Homo sapise 94 8A318628 EST20808 Spleen I Homo sapise 95 16 729112 EST20808 Spleen I Homo sapise 95 16 729112 yu57609.rl Homo sapise 97 18 8A405610 yu52609.rl Homo sapise 97 18 8A405610 EST100987 Pancreas tumor 87 24 8A300891 EST14031 Testis tumor 98 16 8A405478 EST30547 Colon I Homo sapise 97 24 8A32754 EST30547 Colon I Homo sapise 97 25 8A361497 EST30547 Colon I Homo sapise 97 25 8A361497 EST30547 Colon I Homo sapise 97 25 8A361497 EST30547 Testis tumor 97 25 8A361497 EST30547 Testis tumor 97 25 8A361497 EST30547 Colon I Homo sapise 97 25 8A361497 EST30547 Testis tumor 97 25 8A361	4	כמ	3 62	2 63	1 63	0 63	9 63	63	7 64	6 64	5 64	4 65	3 65	2 66	1 66	0 66	9 66	8 67	7 68	6 69	5 69	4 69	3 70	2 70.	1 72	0 73	9 74	8 74	7 75	6 76	15 76 2	4 /6
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1936 vq50c10.r1 Sac Say 10,261 EST1505 Gall 1251 EST1505 Gall 1521 then 1532 vg450c10.r1 Bat 1532 sq. 46h01.r1 Hon 154 Sq. 20 sq. 1640 sq. 17 Sac Say 10,264 sq. 1828 EST20808 Splee EST20808 Splee 10049 v44e01.r1 Hon 1632 vg457e08.r1 Hon 1632 vg457e08.r1 Hon 1632 vg457e09.r1 Hon 16447 ve80a03.r1 Sac EST14031 Test 152447 ve80a03.r1 Sac EST10987 Pana 1547 Ve80a03.r1 Hon 1547 Vg5503.r1 Sac	24	10	10	7	16	25	25	vi	ഗ	16	24	24	7	16	10	24	24	œ	16	16	16	1	σı	24	0	25	19	16	4	U	ω	
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	ST13427 Testis tumor	w20fl1.rl Soares ova	v33c09.rl Soares ova	7fll.rl Soares ova	99871 Homo	78511 Pancı	71040 T-cel	4h03.r1 Hon	5c03.rl Homo sap	2b04.r1 Homo sap	30547 Colon I	13764 Testis tu	8cl2.rl Soares ov	2h11.r1 Homo sa	80a03.rl Soares	T100987 Pancreas	T14031 Testis tumc	38g06.rl Soa:	22f09.rl Homo	65d05.rl Homo	T69384 Homo :	49e01.rl Barstead	57e08.rl Homo sa	T20808 Spleen I	56d02.rl Soares o	r39457 Esophagus	40h01.rl Homo sapi	82d09.r1 Homo sapie	T14181 Testis tumo	T51505 Gall bladde	50cl0.rl Barstead b	usbbub.rl Soares ova

FEATURES source		TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ACCESSION NID KEYWORDS SOURCE ORGANISM	RESULT 1 LOCUS DEFINITION
Seq primer: -28ml3 rev2 ET from Amersham. Location/Qualifiers .1396 /organism="Mus musculus" /strain="FVB/N" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified	Contact: Marra M./Mouse EST project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI-619473	Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R. The WashU-HHMI Mouse EST Project Unpublished (1996)	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 396) Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,	AA691311 92692247 EST. house mouse. Mus musculus	AA691311 396 bp mRNA EST 16-DEC-1997 vs14f01.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone 1138201 5' similar to gb:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                             Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Euther Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 344)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub Geisel,S., Kucaba,T., Lacy,M., Le,M., Marrin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA592800 344 bp mRNA 17-SEP-1997 vo25911.r1 Barstead mouse irradiated colon MPLRB7 Mus musculus clone 1050980 5' similar to 9b:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                             Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                              Waterston, R.
The WashU-HHMI Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g2406463
                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                        Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
/1ab_host="DH10B" 94 t
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89.6%;
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Pred. No. 0.00e+00;
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Best Local S
Matches 22
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                                                                                                                                                                                                                                                                                                                                                                                                                             CCACTTATTACTGCCAGCAGTGGAGTCGTA 281
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                                        Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 345)

1 (bases 1 to 345)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Marrin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                               vt53a04.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone 1166766 5' similar to gb:X02484_rnal IG KAPPA CHAIN PRECURSOR V-IV REGION (HUMAN); gb:J00560 mouse ig kappa mrna from mopc2l & other myeloma mrna 3' (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other myeloma
AA710291
              The WashU-HHMI Mouse 
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                       AA710291
                                                                                                                                                                                                                                              g2720209
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larity 83.7%;
Conservative
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/db_xref="taxon:10090"
/clone="105980"
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/dev_stage="8 weeks"
/lab_host="DH10B"
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Pred. No. 0.00e+00;
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                                                  AA318377 335 bp mRNA EST 19-APR-1997 EST20620 Spleen I Homo sapiens cDNA 5' end similar to similar immunoglobulin kappa light chain, V region, anti-thyroglobulin (GB:X79786), mRNA sequence.

AA318377
B1970863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 140. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                     human
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/db_xref="taxon:10090"
/cl_pra=="146777"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained from 8 week old mouse. (Colon was harvested 72 hours after irradiation with 1400 Gys. 1st strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
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/strain="FVB/N"
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Pred. No. 2.27e-131;
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  272
                                                                                                                            156 TTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTTGCAACTTACTACTGTCAACAG 215
                                                   216 AGTTCCAGTAGCCCTTGGACGTTCGGCCAAGGGNCCAAGGTGGCAATCAA 265
                                                                                                    212 TACTCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAG
                                                                                                                                                                                                                                                               96
                                                                                                                                                                                                                                                                                                             92 AGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAACCTTGGATTTATACC 151
                                                                                                                                                                                                                                                                                                                                                              36 AGCTATTTACATTGGTATCAGCACAAACCAGGTAAAGCCCCCTAAACTCCTGATCTATGNT 95
                                                                                                                                                                                                         ACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGTGGGGTCTGGGACCTCT
TGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGTCCAAGCTGGAAATAAA
                                                                                                                                                                                                                                                       ACATCCACTTTGCAAAGTGGGGTCCCCATCAAGGTTCAGTGGCACTGGATCTGGGACAGAT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
White, O., Sutton, R.R., Cotton, M.D., Earle-Hughes, J., File, L.D.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., File, L.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
155; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: spleen; Vector: pBluescript SK-; Site_1: Ecorl; Site_2: XhoI"
/db_xref="ATCC (inhost):119058"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Spleen I"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ∕organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                26.28;
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88 c
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Pred. No. 3.89e-
1; Mismatches
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.2%;
Best Local Similarity 68.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                 292 TGAAGATGTTGCAACTTACTACTGTCAACAG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 CCTCACTTGCCGGGCAAGTCAGAGCATTAGCACCTTTTTAAATTGGTATCAGCAGAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 AATGACTTGCAGGGCCACCCCAAGTGTAAGTTACATGC---ACTGGTATCAGCAGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGT-CAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GACCTGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., Kelley, J.M., Kilmek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrite, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Melssner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of CDNA Sequence
                                                                                                                                               TCGCTTCAGTGGCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGC
                                                                                                                                                                                                 AAGGTTCAGTGGCTCTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACC
                                                                                                                                                                                                                                                                                                                                                                                           AGGGACAGCCCCTAAGCTCCTGATCTCTGCTGCATCCAATTTGCGAAGTGGGGTCCCATC
                                                                                                                                                                                                                                                                                                                   AGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGC
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EST100653 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20 Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Date of the trick of the trick
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ost
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Venter, JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (tdbinfo@tdb.tigr.org)
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113 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 81; DB 16; Le
Pred. No. 4.41e-111;
1; Mismatches 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                  348
                                                                                                        288
                                                                                                                                     152 ACATCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGTGGGTCTGGGACCTCT
                                                                                                                                                                           228
                                                                                                                                                                                                                                           168 AGTTATTTGGATTGGTACCTGCAGAAGCCAGGACAGTCTCCACAGCTCCTGATCTATTTG 227
                                                                                                                                                                                                        92 AGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAACCTTGGATTTATATACC
                ACTCTACAGACCCCGCTCACTTTCGGCGGAGGGACCAAGGTNGAGAT 394
                                                                 TACTCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAG
                                                                                     GCTTCTAAGCGGGCCTCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGAT 287
TGGAGTCGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAAAT
                                                                                                                                                                                                                                                                              24.9%;
l Similarity 67.0%;
152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; IMAGE Consortium (info@image.llnl.gov) for further :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yl48g05.rl Homo sapiens cDNA clone 161528 5' similar IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN);. H25625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 488)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-Merck EST Project 
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Os;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/clone="161528"
130 c 128 g 12
                                                                                                                                                                                                                                                                                                                                                                                                                            1. .488
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                              Score 80; DB 16; I
Pred. No. 4.53e-109;
1; Mismatches 74;
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                                                                                                                                           GCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCC
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EST13847 Testis tumor Homo sapiens cDNA 5' end similar to similar to immunoglobulin Kappa light chain (GB:S49006), mRNA sequence AA300732 g1953300 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vy54b07.rl Stratagene mouse lung 937302 Mus musculus cDNA clone 1299253 5' similar to gb:x67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.
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1 (bases 1 to 194)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuc Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                    Similarity
99; Conse
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                                                                                                                                                                                                                                                                24.6%;
larity 86.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="lung"
/dev_stage="6-8 month old"
/lab_host="SOLR (kanamycin resistant)"
54 c 39 g 47 t
                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Stratagene mouse
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                               Score 79; DB 14; L
Pred. No. 4.61e-107;
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                                                                                                                                                                                                     103
                                                                                                                                          163
                   283
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                                                                                                                                                                                                                                                                  148;
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Mai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Frichman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Colenan, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
CCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAAATAAA
                                                    CCCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 221
                                                                                                                   AGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTCGTAG
                                                                                                                                                                              CATCAGCAGCCTGCAGCCTGAAGATTTTGCCAACTTACTATTGTCAACAGGCTAACAGTTT
                                                                                                                                                                                                                                                   KGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGTGGGTCTGGGACCTCTTACTCTCTCAC
                                                                                                                                                                                                                                                                                                              GCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCAC 122
                                                                                                                                                                                                                                                                                                                                                                             CTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCT
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Other_ESTs: THC87411
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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ECORI, Ste_2: XhOI"
/db_xref="ATCC (inhost):192041"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult" <1. .>333
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No. 4.61e-107;
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                                                                                                                                78 GACATTCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACAGAGT-CAC 136
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

AL Nature 377 (6547 Suppl), 3-174 (1995)
AATGACTTGCAGGGCCACCC--CAAGTGTA-AGTTACATGCACTGGTATCAGCAGAAGCC
                                            CATCACTTGCCGGGCTGGGCAGCACATTAACACCTATTTAAATTGGTATCAACAGAAACC 196
                                                                                                       GACCTGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACAC 63
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Eukaryotae; π
Vertebrata; ν
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AA301347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kerlavage, AR
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 3018699423
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA301347 413 bp mRNA EST 18-APR-1997 EST14279 Testis tumor Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa light chain, V region (GB:L01279), mRNA
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                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: testis; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):191658"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Testis tumor"
                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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Pred. No. 4.61e-107;
1; Mismatches 104;
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                                                                                                                                                                                                                 Mismatches 104;
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REFERENCE
AUTHORS
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
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Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Frister, C.M. and Venter, J.C.
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                           Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                  Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
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/note-"Organ: thymus; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):191388"
/db_xref="taxon:9606"
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                                                                                                          /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                      Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
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Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTCGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATCAGCAGCCTGCAGTCTGAAGATTTTNCAGTTTATTACTGTCAGCAGTATAAAAACTG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGTGGGGTCTGGGACCTCTTACTCTCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCAC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGTATCAGCAGAAGCCAGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGTACCAGCAGAAACCTGGCCAGGNTCCCAGGCTCCTNATCTATGGTGCATCCACCAG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCAGAGACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 231
                                                                                                                                                                                                                                                                                   Nature 37
96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146;
  Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST100400 Pancreas
                                                                                                                                                                                                                                                                                                 Initial assessment of human gene diversity and expression based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                   Fax: 3018699423
                                                                                                                                                               9712 Medical Center Drive,
                                                                                                                                                                                     The Institute for Genomic
                                                                                                                                                                                                               Bioinformatics
                                                                                                                                                                                                                                                           Other_ESTs: THC168243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similar to
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Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 370)
primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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<1. .>253
% 69 c 65 g
                                                                                                                                                                                                                                  Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin kappa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bp mRNA EST 18-APR-1997
tumor I Homo sapiens cDNA 5' end similar to
lobulin kappa, variable region (GB:Y00640), mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
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                                                                                                                                                                                       Research
                                                                                                                                                            Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24;
4.66e-105;
--hes 72;
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mRNA
BASE COUNT
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                           MEDLINE
                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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                                   Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Colenan, T.A., Collins, E.J.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Colenan, T.A., Collins, E.J.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.E., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of CDNA sequence
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|| |||||||| |||||
GCCACTTATTACTGCCAGCA 270
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EST.
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Other_ESTs: THC169106
                           96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 328)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85
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ECORI; Site_1: XhoI"
/db_xref="ATCC (inhost):190705"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
<1. .>370
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1. .370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.3%;
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Pred. No. 4.66e-105;
1; Mismatches 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VJ regions, mRNA sequence.
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mRNA
BASE COUNT
ORIGIN
   REFERENCE
AUTHORS
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LOCUS
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Best Local S
Matches 17
                                                                                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCACTTATTACTGCCAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCAGTTTATTACTGTCAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCAGTGGGTCTGGGACAGAGTTCACTCTCANCATCAGCATCCTGCAGTCTGAAGATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGACGCAGNTINCAGCCACCCTGTCTGTGTNTCCAGGGGA-AAGAGCCACCCTNTCCTGC 108
                     Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Os:
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
175; Conse
                                                                                                                                       double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento
                                                                                                                                                                                                        R69482 210 bp mRNA EST yj83c03.rl Homo sapiens cDNA clone 155332 5 IG KAPPA CHAIN V-I REGION (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  information related to this EST, please check the TIGR Human Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse.
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The Institute
                                                                                                                            Soares and M.Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kerlavage,
theria; Archonta; Primates;
(bases 1 to 210)
llier,L., Clark,N., Dubuque,
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/db_xref="ATCC (inhost):190766"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Pancreas tumor
/dev_stage="adult"
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Dubuque, T.,
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. 4.67e-103;
.~hes 82;
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 Elliston, K., Hawkins, M.
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5' similar to gb:L0
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                                                                    Hillier, L., Allen, M., Bowles, L., Dubuque, T., Ge:
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., 1
White, Y., Wylle, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                              AA479857 242 bp
zu35b05.rl Soares ovary
5' similar to gb:X06764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality.
Location/Qualifiers
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           Washington University Sch
4444 Forest Park Parkway,
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AA479857
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Fax: 314 286 1810
                                             Contact: Wilson
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                                                                                                                                                                                                         Vertebrata;
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Parsons,J., Rifkin,L., Rohlfing,T., Soare
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314 286
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/clone="155332"
56 c 46 g 5
                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                        mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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Pred. No. 4.64e-101;
1; Mismatches 60:
           School of Medicine way, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                 tumor NbHOT Homo sapiens cDNA clone 7: IG KAPPA CHAIN PRECURSOR V-III REGION
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             Louis,
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                                                                                                                                          Martin, J
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                                                                                                                                                                                                                                                                                                                       AA869306
92964751
EST.
                                                                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 276)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuq
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                               AA869306 276 bp mRNA EST 16-MAR-1998 vq50c10.rl Barstead bowel MFLBB9 Mus musculus cDNA clone 1097682 similar to gb:x67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE); mRNA sequence.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham.
                                                                              Unpublished (1996)
                                                                                                 Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                     house mouse.
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/clone="739953"
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66 c 69 g
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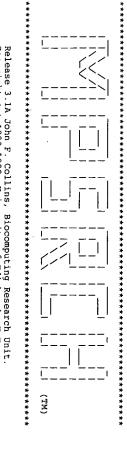
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Best Local Similarity 83.9%;
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                                 ACTATGGATTTATTACACATCCAAC-TGGCT-CTGGAGTCC
                                                                                                   GGC-AGCTCAAGTGTAAATTACATGTACTGGTACCAGCAGAAGTCAGATGCCTCCCC-AA 237
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ACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCC
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Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:603914
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/dev_stage="8 weeks"
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/tissue_type="bowel"
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63 c 59 g
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/clone="1097682"
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat Jan 9 15:15:33 1999; MasPar time 533.48 Seconds 1437.582 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-08-704-178-1 (364-711) from US08704178.seq (3 of 4) 348 364 TGTGCAGCTGCAGGAGTCAG.......GGGACCACGGTCACCGTCTC ACACGTCGACGTCCTCAGTC.......CCCTGGTGCCAGTGGCAGAG

711

Nmatch STD : Gap Dbase 0; Query 0 TABLE default Gap 6

Scoring table:

Searched: 567134 seqs, 1101898692 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database:

emb155
1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl
13:em_ro 14:em_vi
genbank107
15:gb_ba1 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov
21:gb_pat 22:gb_ph 23:gb_pl1 24:gb_pl2 25:gb_pr1
26:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 30:gb_sts 31:gb_sy
32:gb_un 33:gb_vi

Statistics: Mean 9.880; Variance 4.986; scale 1.981

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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S75677	E07407	MUSIGHZZH	MMAFBPOVH	S54755	MMIGPE15	MUSIGHAPA	MMBV1619H	MUSANTDNAS	MMVH343C	MUSIG438A	MMU60457	MMVAR609	I45604	MUSIGGVDJB	MMIGHT110	MUSIGHAAV	MMVAR604	MUSIGHCP	AF083188	MDIGMVAE	MUSIGHAB	MUSIGKCLS	MUSHA3	MUSIGHI	AF004402	MUSIGGVDJE	MMU28805	E07912	MMU88682	4	AFUSI541
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AUTHORS King C.Richter, Kasprzyk,P.G. and Bird,R.E. TITLE data antibodies, combinations thereof, and therapeutic diagnostic uses thereof JOURNAL Patent: US 5587458-A 1 24-DEC-1996; ATURES Source 1. 711 SE COUNT 175 a 182 c 190 g 164 t IGIN 175 a
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/translation="MDLQLTQSPAILSASPGEKVTMTCRATPSVSYMHWYQQKPGSSPKPWIYTTSNLASGVPARFSGGSGTSYSLTVSRVEADATYYQQWSRSPPTFGGGSKFIYTTSNLASGVPARFSGGSGTSYSLTVSRVEADATYYCASKPETMMVKQSKLEIKGSTSGSKSSEKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMMVKQSHGKNLEWIGLINPYNGTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRYTDWYFDVWGAGTTYTYS"
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/note="This sequence comes from Fig. 1."
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rođentia; Sciurognathi; Myomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-OCT-1995) Jennifer R. Swartzentruber, Institute, 3601 Spruce St., Philadelphia, PA 19104, Location/Qualifiers
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96136744
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                                                                                                                                                                                                                                                                      308;
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Swartzentruber, J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caton, A.J., Swartzentruber, J.R., Kuhl, A.L., Carding, S.R.
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/translation="ELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWIGLINP
YNGGTSYNQKFKGKATLTVDKSSSTAYMELLSLTSEDSAVYYCAREWLLRYFDVWGAG
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/isolate="h922-163"
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Pred. No. 7.81e-203;
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CAGAAGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATG
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Ig VH-anti-phosphatidylserine monclonal variable region [mice, hybridoma, mRNA i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complementarity determining region to J. Biochem. 117 (2), 452-457 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus.
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larity 90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  is in conflict with the conceptual translation; mismatch(35[K->N])"
                                                                                                                                                                                                                                                                                                                  /product="anti-phosphatidylserine monclonal antibody PS4A7 heavy chain variable region" /db_xref="pID:g1041921" /db_xref="pID:g1041921" /translation="EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMKWVKQSHGKN /translation="EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMKWVKQSHGKN LEWIGLINPYNGGTSYNQKFKGKATLTVDKSSSTAYMELLSLTSDDSAVYYCAREGDY DGAMDYWGQGTSVTVS" 82 t
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heavy chain variable region"
, gene_"Ig VH"
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Cloning and sequencing of immunos
by polymerase chain reaction
Sheng Wu Hua Hsueh Tsa Chih 9 (No
2 (bases 1 to 351)
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Submitted (21-APR-1995) Lin Xu, Institute
Sinica, Dept. of Protein Engineering, 15 D
District, Beijing 100101, Peoples Republic
Location/Qualifiers
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/label=JC1077
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/product="immunoglobulin heavy chain variable region"
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/translation="QVQLQQSGPELVKPGASMKISCKTSGYSFTGYTMN"
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/translation="QVQLQQSGPELVKPGASMKISCKTSGYSFTGYTMS"
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/translation="QVQLQSGPELVKTSGYSTGY"
/translation="QVQLQSGPELVKTSGYSFTGYTMS"
/translation="QVQLQSGPE
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/db_xref="taxon:10090"
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Pred. No. 7.10e-188;
0; Mismatches 31:
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$74055 355 bp mRNA IgG VH IIA=IgG2b VH region [mice, mRNA Recombinant Partial, 355 nt].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-AUG-1995) M. Geiser, K-681.5.46, CH-4002, Basel, SWITZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Geiser, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Vertebrata; Eutheria; Rodentia; Sciurognathi; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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/db_xref="taxon:10090"
/dev_stage="12 weeks old"
/tissue_type="spleen"
/cell_type="lymphocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Codon_start=1
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LEWIGDIMPNNGDTFYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCANDGYH
MYFDVWGAGTPVTVSS"
#YFDVWGAGTPVTVSS"
89 c 93 g 80 t
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89.1%;
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Pred. No. 3.24e-186; 
0; Mismatches 36; Indels
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                                                                     GACTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTC
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Mount.P.F., Sutton,V.R., Li,W., Burgess,J., McKEnzie,I.F.,
Pietersz,G.A. and Trapani,J.A.
Chimeric (mouse/human) anti-colon cancer antibody c30.6 inhibits
the growth of human colorectal cancer xenografts in scid/scid mice
Cancer Res. 54 (23), 6160-6166 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenBank staff at the National Library of Medicine created this entry [NCBI glbbsq 157470] from the original journal article. This sequence comes from Fig. 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae;
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llarity 87.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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LEWIGFIYPYNAGTGYNQKFKNKATLTVDSSSSTAYMELRSLTSEDSAVYYCTRNDPH
WYFYVWGQGTTVVVSS"
90 9 80 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="chimeric anti-colon cancer monoclonal antibody c30.6/IgG heavy chain variable region; chimeric mouse/human. This sequence comes from Fig. 1A"
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1. .354
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/gene="IgG V<down>H</down>
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Eutheria; Rodentia; Sciurognathi; I
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Pred. No. 1.00e-183;
0; Mismatches 44;
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DEFINITION

Mouse mRNA sequence,

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Best Local Similarity 89.18;
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178572
g3014726
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Simpson,J.A., Chow,J.C., Baker,J., Avdalovic,N.M., Co,M.S., Vasquez,M., Britt,W.J. and Coelingh,K.L. Untitled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M95944
g309176
                                                                Queen,C.L., Schneider,W.P. and Selick,H.E. Polynucleotides encoding improved humanized Patent: US 5693761-A 84 02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (strain BALB/c, sub_species domesticus) cDNA Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; N
                                                                                                                          Unclassified
                                                                                                                                                       Unknown.
                                                                                                                                                                                                                          178572
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                                                                                                         (bases 1 to 414)
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87 c 88
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/db_xref="taxon:10090"
/cell_line="MAb 5"
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/strain="BALB/c"
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1. .357
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Pred. No. 1.00e-183;
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            GAGCTCCTCAGTCTGACATCTGCGGACTCTGCAGTCTATTACTGTACAAGACGGGGGTTT
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178627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown
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Similarity 89.1%;
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Patent: US 5693762-A 84 02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                and Selick, H.E.
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                                                                                                                                                                                                                                                                                                                                                                                     TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT 484
         1 (bases 1 to 421)
Takahashi, S., Matsuura, Y., Taniquchi, T., Tamura, H
Onishi, S., Yamamoto, Y., Yamamoto, H. and Fujimoto,
Molecular analysis of immunoglobulin heavy chain
idiotypic and anti-idiotypic antibodies involved
interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l (bases 1 to 414)
Oueen, C.L. and Selick, H.E.
Humanized immunoglobulins
Patent: US 5585089-A 84 17-DEC-1996;
Location/Qualifiers
                                                                                                        Mus sp.
Eukaryotae;
                                                                                                                                                                                       M104E myeloma
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                                                                                               Vertebrata;
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larity 89.1%;
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102 c 103 g
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                                                                                          mitochondrial eukaryotes; Metazoa; Chordata; Eutheria; Rodentia; Sciurognathi; Muridae; M
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Pred. No. 1.00e-183;
0; Mismatches 35;
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                                             Tamura,H., Bitoh,S.,
Fujimoto,S.
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          Direct Submission
Submitted (24-NOV-1997) LMB, N
4B20, Bethesda, MD 20892-4255,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310;
                                                2 (bases 1 to Chowdhury, P.S.
                                                                                       Rodentia; Sciurognathi;
1 (bases 1 to 723)
Chowdhury, P.S.
SS scFv
                                                                                                                                                                                                          Mus musculus
AF035617
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Location/Qualifiers
                                                                                                                                         Eukaryotae; Metazoa;
                                                                                                                                                         Mus musculus
                                                                                                                                                                                             g2921393
                                                                          Unpublished
                                                                                                                                                                       house mouse.
                                                                                                                                                                                                                                   AF035617
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Similarity 89.38;
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segment are shown completely;
partially"
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100 c 113 g 102 t
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GYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSYNQKFKGKATLTVDKSSSTAYMQL
Location/Qualifiers
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/db_xref="taxon:10095"
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SCFV
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antibody
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Pred. No. 6.75e-183;
0; M1smatches 34:
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AF081541
                     Direct Submission
Direct Submission
Submitted (01-AUG-1998) Functional Biomolecules, Unilever Research
Submitted (1998) Functional Biomolecules, Unilever Research
Submitted (1998) Functional Biomolecules, Unilever Research
                                                                                  Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 366)

de Haard, J.J.W., Kazemier, B., Koolen, M.J.M., Nijholt, L.J.,
Meloen, R.H., van Gemen, B., Hoogenboom, H.R.M. and Arends, J.W.
Selection of recombinant, library derived antibody fragments
against p24 for application in HIV-1 diagnostics
clin. Diagn. Lab. Immunol. (1998) In press
clin. Diagn. Lab. Immunol. (1998) Glases 1 to 366)

de Haard, J.J.W., Kazemier, B., Koolen, M.J.M., Nijholt, L.J.,
Meloen, R.H., van Gemen, B., Hoogenboom, H.R.M. and Arends, J.W.
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                 Laboratorium Vlaardingen, 3133 AT, The Netherlands
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/db_xref="plD:y292139"
/db_xref="plD:y292139"
/tanslation="MOYOLOOSGPELEKPGASYKISCKASGYSFTGYTMNWVKOSHGK
/translation="MOYOLOOSGPELEKPGASYKISCKASGYSFTGYTMNWVKOSHGK
SLEWIGLITPYNGASSYNOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGY
BCRGFDYWGOGTTVTVSSGVGGGGGGGGGGGSDIELTOSPAINSASPGEKVTMYCSA
SSSVSYMWYQOKSGTSPKRWIYDTSKLASGYPGRFSGSGSGNSYSLTISSVEAEDDA
TYYCOOWSGYPLTFGAGTKLEIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
/tissue_type="spleen"
/clone_lib="phage display library made from spleen mRNA
mice immunized with DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                             Metazoa; Chordata; Vertebrata;
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. No. 4.56e-182;
Mismatches 36;
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A2 Ig heavy
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                                                                                                                                                                                                                                                         1 (bases 1 to 440)
Rueff-Juy, D., Marche, P.N., Drapier, A.-M. and Cazenave, P.-A.
Junctional diversity of H and L chains allows the coexpression
two mutually exclusive idiotopes (IdII04 and IdI558)
                                                                                                                                                                                                                                                                                                                                                                           g193744
J-region; V-region; immunoglobulin
Mus musculus cDNA to mRNA.
                                                                                                                                                                                                                               J. Immunol. 146, 4024-4030 (1991) 91237115
                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondr
Vertebrata; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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 Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain variable region"
/db_xref="piD:g3493269"
/db_xref="piD:g3493269"
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/translation="QVQLQQSGKATLTVDKSSSTAYMELLSLTSEDSAVYYCARDPYY
YGSSWYFDVWGAGTPVTVSS"
a 91 c 95 g 89 t
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/strain="BALB/c"
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/nofe="immusi---
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regions"
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/cell_line="hybridoma"
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"anti-HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="immunized with HIV-1
                                                            /db_xref="PID:g193745"
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93.8%;
                                                                                                                                                                                                                                                                                                                                   mitochondrial eukaryotes; Metazoa;
Eutheria; Rodentia; Sciurognathi; )
                                                                                                                                                                                                                                                                                                                                                                                                                                              440 bp
H-chain
 112 c
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Pred. No. 6.36e-178;
0; Mismatches 18:
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110 g
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region,
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Search completed: Sat Jan 9 15:24:33 1999 Job time: 540 secs.
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                                                                                                                                                                                                                                                                              Query Match 71.8%; Score 250; DB 28; Length 440; Best Local Similarity 88.2%; Pred. No. 2.88e-176; Matches 306; Conservative 0; Mismatches 38; Indels 3;
                                                                            273 CAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 332
                                                                                                                                                                                                665 GACTGGTACTTCGATGTCTGGGGCGCGCAGGGACCACGGTCACCGTCTC 711
                                                 391 -ACTGGTACTTCGATGTCTGGGGCACAGGGACCACGGTCACCGTCTC 436
                                                                                                                                                                                                                                                                                Gaps
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Releas	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
srch_nn n.a	n.a. database search, using Smith-Waterman algorithm
n on:	Sat Jan 9 16:26:30 1999; MasPar time 64.16 Seconds
oular output n	oular output not generated.
tle: scription:	>US-08-704-178-1 (364-711) from US08704178.seq (3 of 4)
A. Sequence:	364 TGTGCAGGAGGAGTCAGGGGACCACGGTCACCGTCTC 711 ACACGTCGACGTCCTCAGTCCCCTGGTGCCAGTGGCAGAG
oring table:	TABLE default Gap 6

Tit Des Per N.A Sco Nmatch STD: Dbase 0; Query 0

Tab Run

MPS

Database: Post-processing: Minimum Match 0% Listing first 45 summaries Searched:

188442 seqs, 68026449 bases x 2

n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 23:part23
29:part29 30:part20 31:part31 32:part32 33:part133
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 8.057; Variance 4.765; scale 1.691

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	BB	Ħ	Description	Pred. No.
_	348	100.0		29	T65006	Single-chain anti-erb	4.40e-225
2	344	98.9	711	18	T17728	Anti-erbB2 scFv cDNA.	3.29e-222
ω	344	98.9		9	Q55180	Sequence encoding the	3.29e-222
4	265	76.1	462	22	T34542	Monoclonal anti-idiot	1.26e-165
5	265	76.1	462	21	T31541	3H1 heavy chain varia	1.26e-165
o	265	76.1	462	38	T99435	Anti-idiotype antibod	1.26e-165
7	257	73.9		7	Q43843	Chimeric 128.1 VH, mo	6.39e-160
æ	257	73.9		7	Q43846	Plasmid pAH4625.	6.39e-160
ø	257	73.9		7	Q43848	Plasmid pAH4808.	6.39e-160
10	257	73.9		7	Q43844	Plasmid pAH4602.	6.39e-160
11	257	73.9		7	Q43847	Plasmid pAH4807.	6.39e-160
12	249	71.6		11	Q45428	KM-750 heavy chain.	3.21e-154
13	245	70.4		5	Q28522	Hypercalcaemia agent	2.27e-151

																														15	
212	212	212	212	213	215	217	217	217	218	219	220	221	221	221	222	224	225	225	225	225	225	225	225	230	231	231	235	235	240	242	242
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T7859	T0338	Q1129	T7858	T5825	T0401	T5933	Q2714	T0401	T3415	V0979	V0979	20469	T3129	T0501	V2060	T4271	Q1205	Q1201	Q3075	T1261	Q6993	T4373	T4373	Q7367	T8886	Q4542	Q7037	Q6555	Q8107	7 T86311	T8630
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meric		Encodes n	Monoclona	o.	Anti-EGFR	mon	ICAM-1 ir	Anti-EGFR antibody	Monoclonal	DNA encoding	DNA encod	Heavy cha	Guy's 13	anti	7 anti	MC3 VH		Sequence	12-h2.	'v U7.	.6 heav	i-DNA	-DNA	,	₽.	KM-796 he	۷IH	ant	ispecific	ingle ch	le c
monoc		murine m	ıl antib	Ĕ	16	ĕ	inhibiting	≀ antibo	ıl antibody	ling the	#	ar	·-st	body hea	Fc alpha	coding s	encoding	encoding		6 VH gene	chain	tibod	antibody		n subunit o	eavy chain	tibo	VIH	CB3	n ant	in ant
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.25e-1	.25e-1	.25e-1	.25e-1	.22e-1	.68e-1	.79e-1	.79e-1	.79e-1	.49e-1	.82e-1	.33e-1	.60e-1	.60e-1	.60e-1	.07e-1	.93e-1	.76e-1	.76e-1	.76e-1	.76e-1	.76e-1	.76e-1	.76e-1	.06e-1	.06e-1	.06e-1	.95e-1	.95e-1	.21e-1	L	.10e-1
28	28	28	28	28	30	31	31	31	32	33	ω ω	34	34	34	35	36	37	37	37	37	37	37	37	40	41	41				49	

88888	88	6	CC	ΡŢ	P P	DR	DR	P	PA	υ :	ָאָל ;	PR	PF	PD	PN	Ϋ́	Ϋ́	FΤ	FΗ	SO	သူ	XW	XX	K₩	DE	Ŋ	ΑC	Ĭ	RESULT
by standard techniques. Messenger RNA coding for the anti-erbB-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light- chain variable regions were then amplifted by PCR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro	was generated by immunising mice with N/erbB-2 cells overexpressing the gpl85 protein, removing spleen cells and producing hybridomas	ignated e23(Fv), which binds	Example 8; Columns 25-28; 28pp; English. The present cDNA sequence codes for a claimed single-chain antibody,		labels or cytotoxin, useful for detection and treatment of tumour	W15185.	64831/06.	Bird RE. Kasnrzyk PG. King CR.	Πi .		30-710-1992: 178-906555		07-OCT-1991; 772270.	24-DEC-1996.		/product= e23(Fv)		mat_peptide 1711	Key Location/Qualifiers	Synthetic.	•	diagnosis; treatment; cytotoxic ag	r; ovarian cancer; non-small cell	Single chain antibody; variable region; light chain; heavy chain;	anti-e	05-JUN-1997 (first entry)		T65006 standard; cDNA; 711 BP.	LT 1

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RESULT ACCORDED TO A CONTROL OF THE PROPERTY O
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          Query Match
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Best Local S
Matches 34
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Synthetic.
W09607321-A1
14-MAR-1996
23-AUG-1995; U10740.
06-SEP-1994; US-301339.
06-JUN-1995; US-468252.
(UABR-) UAB RES FOUND.
Curiel DT, Deshane J;
WPI; 96-171307/17.
                                                                                                                                                                                            P-PBDB; R94020.

Inhibition of proliferation or survival of, esp. malignant erbB2, cells by introducing nucleic acid mol. encoding antibody homologue which is expressed and binds, pref. erbB2, protein intracellularly Claim 42; Page 29-30; 48pp; English.

A nucleic acid comprises a first sequence encoding a signal peptide (R94019) linked to a second sequence (T17728) encoding a single chain Fv fragment (R94020) that binds a human erbB2 oncoprotein. The anti-erbB2 sFv portion is obtained by PGR using e23scFv plasmid as template. The signal peptide directs the scFv to the endoplasmic reticulum. The nucleic acid is incorporated into a plasmid or viral vector to facilitate expression of the scFv antibody homologue within e.g. an epithelial carcinoma cell. Intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T17728
T17728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncoprotein; erbB2; cell proliferation; tumour; cancer; intracellular antibody homologue; single chain antibody; scFv;
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                                                                                                         tumorigenicity.
Sequence 711
                                                                                                                                                        expression of the homologue inhibits surface expression thereby inhibits cell proliferation and cell survival an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-erbB2
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          346;
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Similarity 100.0%;
348; Conservative
                                 Similarity
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          Conservative
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                                 98.9%;
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Score 348; DB 29;
Pred. No. 4.40e-225;
0; Mismatches 0;
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                                                   Length 711;
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Best Local S
Matches 34
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WPI; 94-025878/03.
P-PSDB; R45442.
Treatment of malignancies over-expressing ERB-[2 - using at
"monoclonal antibodies which recognise different epitopes (
                                                                                                                                                                                  Example; Fig 7; 37pp; English.

The source of human erbB-2 protein for the prodn. of antibodies n 23 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. animals given a combination of the 2 Abs, tumours completely regressed after 11 days.

Sequence 711 BP; 175 A; 183 C; 187 G; 165 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monoclonal antibody; ss. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1994 (first entry)
Sequence encoding the single chair
Single chain anti-erbB1 antibody;
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06-JAN-1994.
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Q55180 standard;
Q55180;
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30-JUN-1992; US-906555.
(MOLE-) MOLECULAR ONCOLOGY
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                                                                                                                                        h 98.9%;
Similarity 99.4%;
346; Conservative
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1..171
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                                                                                                                                      Score 344; DB 9
Pred. No. 3.29e-
0; Mismatches
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cancer therapy; preve
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3.29e-222;
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Best Local :
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28-DEC-1995; U17105.
28-DEC-1994; US-365484.
(KENT ) UNIV KENTUCKY.
Chatterjee M, Chatterjee
MPI; 96-321809/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T34542 standa
T34542;
T34542;
11-OCT-1996
                                                                                                                                                                                                                                                                                                                         to carcinoembryonic antigen
Example 2; Fig 2A; 102pp; English.
A cDNA clone (T34542) codes for the heavy chain variable region
(R99687) of monoclonal anti-idiotype antibody 3H1 (ATCC HB 12003
It was obtd. by PCR amplification (see also T34543-44) of cDNA
derived from 3H1 hybridoma cells. Anti-idiotype antibody 3H1
elicits a specific immune response to a unique epitope of
carcinoembryonic antigen (CEA) that is not present on other
members of the CEA family or on normal adult tissues. 3H1
can be used as a vaccine to elicit immune responses in pattents
with advanced CEA-associated disease or, when labeled, to enhanc
                                                                                                                                                                                                                                                                                                     tumour detection in imaging.

106 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-007-1996 (first entry)
Monoclonal anti-idiotype antibody 3H1 VH cDNA.
Anti-idiotype antibody; monoclonal antibody; CEA;
carcinoembryonic antigen; tumour-associated antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal anti-idiotype antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R99687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immunotherapy; ss.
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90.0%;
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                                                                                                                                                                                                                                                    Score 265; DB 22;
Pred. No. 1.26e-165;
0; Mismatches 32;
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                                                                                                                                                                                                                                                                             Length 462;
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RESULT
ID 731541;
AC 731541;
AC 731541;
DT 18-SEP-1
DT 18-SEP-1
DE 3H1 head
KW Anti-idd
KW carcines
KW vaccines
KW Carcines
KW Carcines
KW Carcines
CA ACDA
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PT CAS
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                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PT Recombinant monoclonal anti-idiotype antibody 3H1 sequences - used to develop prods for the detection and treatment of carcinoembryonic antigen-associated diseases, partic. cancers PS Claim 6; Fig 2A; 121pp; English.

CR A CDNA clone (T31541) codes for the heavy chain variable region (VM) (R98411) of 3H1, a murine monoclonal anti-idiotype antibody that mimics a specific epitope of the 180,000 mol.wt.

CC carcinoembryonic antigen (CEA) and which elicits an immune response in patients with advanced CEA-associated disease, e.g. colorectal cancer. It was obtd. by PCR amplification of 3H1 hybridoma DNA (see also T31545-46). The isolated polynucleotide, and/or a polynucleotide (see also T31540) coding for the VL region (R98410) cof 3H1 can be used to design probes and primers, in expression cystems, and in pharmaceutical applns, including vaccines, gene thorapy and genetic immunisation, partic. against cancer.

Sequence 462 BP; 106 A; 124 C; 117 G; 115 T;
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Best Local S
Matches 31
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Anti-idiotype; monoclonal antibody; MAb; 3H1; CEA; carcinoembryonic antigen; cancer; gene therapy; imm vaccine; genetic immunisation; heavy chain; VH; ss.
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04-JUL-1996.
28-DEC-1995; U17103.
28-DEC-1994; US-365484.
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WPI; 96-321850/32.
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     ACGGACTGGTACTTCGATGTCTGGGGGCGCAGGGACCACGGTCACCGTCTC
                               ccctactggtacttcgatgtctgggggcgcaggggaccacggtcaccgtctc
                                                                                                          GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTG-CA--AGGAGGGTT
                                                                                                                                            gagctcctcagtctgacatctgaggactctgcagtctattactgtgtcattactccggtt
                                                                                                                                                                                                                                                                                                                                    GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCC
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Similarity 90.0%;
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Pred. No. 1.26e-165;
0; Mismatches 32;
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PS Disclosure; Page 39; 66pp; English.

This cDNA sequence includes a coding region for the heavy chain variable region (VH) (see W26729) of murine monoclonal anti-idiotype antibody 3H1. A cDNA sequence (see T99434) for the VL region (see W26728) is also provided. These clones can be utilised in the recombinant production of 3H1 polypeptides. 3H1 induces a specific immune response against a distinct and specific epitope of carcinoembryonic antigen (CEA), a tumour-associated antigen. The invention provides methods of delaying development of CEA-associated tumours using 3H1, particularly in high-risk individuals. The method can be used to delay the development of a variety of tumours, other adenocarcinomas such as those of the breast and lung, and biliary cancer, and gynaecological cancers.

Sequence 462 BP; 106 A; 124 C; 117 G; 115 T;
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Best Local S
Matches 31
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23-OCT-1997; U05953.
11-APR-1997; US-631085.
12-APR-1996; US-631085.
(KENT) UNIV KENTUCKY.
Chatterjee M, Chatterjee Si
WPI; 97-256218/48.
P-PSDB; W26729.
                                        Q43843;
Q43843;
  Chimeric 128.1 VH, mouse - Polymerace -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-idiotype antibody 3H1 heavy chain variable region cDNA. Anti-idiotype antibody 3H1; carcincembryonic antigen; CEA; tumour-specific antigen; tumour; colorectal cancer; lung can adenocarcinoma; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T99435 standard; cDNA; 462
T99435;
27-APR-1998 (first entry)
                                                                                                          662
                                                                                                                                                                                          322
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                                                                                                                                                                                                                                                                      ACGGACTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                   315;
                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                      DNA;
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reaction; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                              76.1%;
                                                      417
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Pred. No. 1.26e-165;
0; Mismatches 32;
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subgroup IIB DNA.
mer; PCR; amplify; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 462;
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                                                                                                          711
 heavy;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
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RESULT
ID Q
AC Q
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Best Local Similarity
Matches 302; Conse
O43846;
Q43846;
Q43846;
Q43846;
Q43846;
Q43846;
Q43846;
20-OCT-1993 (first entry)
Plasmid pAH4625;
Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625;
heavy; light; chain; variable; constant; region; anti-human; pAH41
transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-
endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-
diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
Parkinsons disease; Alzheimers disease; SP2/0 cell; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Table 6; Page 57; 151pp; English.

Table 6; Page 57; 151pp; English.

The sequences given in Q43842-43 encode the light and heavy chains, respectively, of the chimeric antibody 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods.

Sequence 417 BP; 108 A; 104 C; 102 G; 103 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUN-1993.
24-NOV-1992;
26-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       light; chain; variable; constant; region; anti-human; transfe receptor; antibody; brain; capillary; endothelial cell; conju neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders
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                                                                                                                                                                                                                                                                                                                                                                                                         ggagagaaccttgagtggattggacgtattaatcctcacaatggtggtactgactacaac
                                                                                                                                                                                                                                                                                                                                                                                           TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT
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US-800458.
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58..417
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 257; DB 7; I
Pred. No. 6.39e-160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ion; anti-human; transferrin;
endothelial cell; conjugate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 417;
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                                                 pAH4808; gamma-2;
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                                   gamma-4;
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                                                              PAH4807;
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The sequences given in Q43846-48 represent the expression vectors capH4625, pAH4807 and pAH4808. These vectors represent the cloning pAH4808. These vectors represent the cloning of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4 respectively, with the variable region of the murine monoclonal cantibody 128.1. These plasmids each encode a chimeric monoclonal cantibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CH1, CH2 and CH3 are derived from a control of the man source. These vectors in combination with the chimeric light chain vector, pAG4611 (see also Q43845), were transfected into SP2/OC cells and clones were isolated. Antibody analysis using biosynthe-citically labelled proteins, immunoprecipitation and SDS-PAGE indicated appropriate bands for the heavy and light chains as well as the cassembled antibody for the gamma-3 and gamma-4 chimeras. No detectable protein was isolated for the gamma-2 transfectants. 128.1 is an anti-cus assembled antibody for the gamma-2 transfectants. 128.1 is an anti-cus assembled in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent concerns and Alrheimers disease. It may also be used for diagnostic seguines of the paramatic constants and all the configurations and the prevent of the paramatic constants. This and all the proteins are also be used to treat or prevent concerns and all primers of the proteins and the proteins are constant through all the proteins.
                                                                                                                                                                                                                                                                      Matches
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                    2088
                                                                                                                                                             1968
                                                                                                                                                                                                                1908 gtccagctgcaacagtctggacctgaactggtgaagcctggagcttcaatgaagatttcc 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-NOV-1992; U10206.
26-NOV-1991; US-800458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; R41707-09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Friden PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unsure
                                                                                                                                                                                                                                                                                                                                                                             Parkinsons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ALKE-) ALKERMES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                       485
                                                                                                                                                                                                365
                                                                                                                                                                                                                                                                                     Local
cagaagttcaaggacaaggcccctttaactgtagacaagtcatccaacacacgcctacatg
                                                                                                                                          tgcaaggcttctggttactcattcactggctacaccatgaactgggtgaagcagagccat 2027
                                                                      ggagagaccttgagtggattggacgtattaatcctcacaatggtggtactgactacaac
                                                                                                                                                                                              GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGAAGCCTGGAGGTTCAATGAAGATATCC 424
                                                   TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT 484
                                                                                                                                                                                                                                                                      302;
                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                            and Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                          10704 BP;
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Sequence not given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4318..4517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= e
/note= "Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= d
/note= "Undefined ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/note= "Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= c
'note= "Undefined ORF1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
/note= "Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          848..2552
                                                                                                                                                                                                                                                                                   73.9%;
                                                                                                                                                                                                                                                                                                                                       2125 A;
                                                                                                                                                                                                                                                                                   Score 257; DB 7; L
Pred. No. 6.39e-160;
                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128.1 VH/CH1 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not given
                                                                                                                                                                                                                                                                                                                                        2189
                                                                                                                                                                                                                                                                                                                                                                        It may also be used
                                                                                                                                                                                                                                                                                                                                       Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the specification
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                                                                                                                                                                                                                                                                                                                                        2130
                                                                                                                                                                                                                                                                                                   Length 10704;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification"
                                                                                                                                                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                          epilepsy,
for diagnostic
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                                                                                                                                                                                                                                                                  Gaps
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RESULT OF THE PROPERTY OF THE 
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The sequences given in 04386.48 represent the expression vectors pAH4625, pAH4807 and pAH4808. These vectors represent the cloning of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4 respectively, with the variable region of the murine monoclonal antibody 128.1. These plasmids each encode a chimeric monoclonal cantibody in which the heavy chain (VH) is derived from a murine course and the sequences encoding CH1, CH2 and CH3 are derived from a human source. These vectors in combination with the chimeric light chain vector, pAG4611 (see also 043845), were transfected into SP2/0 cells and clones were isolated. Antibody analysis using biosynthetically labelled proteins, immunoprecipitation and SDS-PAGE indicated appropriate bands for the heavy and light chains as well as the casembled antibody for the gamma-3 and gamma-4 chimeras. No detectable protein was isolated for the gamma-2 transfectants. 128.1 is an anti-
cused in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent conceptor and disorders eg. brain tumours, AIDS, stroke, epilepsy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q43848;
Q43848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807 transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody conjugates specific for transferrin receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 93-196742/24.
P-PSDB; R41715-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-1991; US-8
(ALKE-) ALKERMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9310819-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkinsons disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pAH48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    545 CAGAAGTTCAAGGGCCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tactattctttggactactggggtcaaggaacctcagtcaccgtctc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACTGGTACTTCGATGTCTGGGGGCGCAGGGACCACGGTCACCGTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA; 10844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 19A-F; 151pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : U10206.
: US-800458.
ERMES INC.
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6336..6635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= e
/note= "Undefined ORF3"
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/note= "Undefined
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/note= "Murine 128.1 VH/human gamma-4 CH1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note- "Undefined ORF1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimers disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..5482
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isease; SP2/0 cell; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORF2"
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                                                                                                                                                                                      No detectable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
W09310819-A.
10-JUN-1993.
24-NOV-1992;
                                                                                                                                                                                                                                                                         Plasmid pAH4602.

Polymerase chain reaction; primer; PCR; amplify; mu heavy; light; chain; variable; constant; region; ant transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy;
                                                                                                                                                                                                                                                                                                                                    Q43844 standard; 1
Q43844;
20-OCT-1993 (fir:
Plasmid pAH4602.
                                                                                                                                            cds
                                                                                                                                                                                                                                 cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4147
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                                                                                     cds
                                                                                                                 cds
                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                  signal_peptide
                                                       unsure
                                                                                                                                                                                                                                                   unsure
                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkinsons and Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                                                                                        665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggagagaaccttgagtggattggacgtattaatcctcacaatggtggtactgactacaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9tccagctgcaacagtctggacctggaactggtgaagcctggagcttcaatgaagatttcc
                                                                                                                                                                                                                                                                                                                                                                                                      GACTGGTACTTCGATGTCTGGGGGCGCAGGGACCACGGTCACCGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                 tactattctttggactactggggtcaaggaacctcagtcaccgtctc 4313
                                                                                                                                                                                                                                                                                                                                                                                                                                                     tycaagycttctgyttactcattcactgyctacaccatyaactgygtyaaycagayccat 4086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTAAGCCTGGAGGTTCAATGAAGATATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGAGGGTTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGAAGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 73.9%;
Similarity 87.0%;
302; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10844
                                                                                                                                                                                                                                                                                                                                               (first entry)
U10206
                           /*tag= 11
8177..8201
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/note= "Leader
3964..4611
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/note= "VH
3097..3963
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3907..4
                                                                                   5589..5909
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/note= "Undefined
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/note= "Undefined
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/note= "Mature
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/note= "Undefined
                                                                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 6.39e-160;
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Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain variable region (VH) of the antibody 128.1, an ampicillin resistance gene and a histidine (histidinol) selection marker. Transcription of the VH gene is from the VH promoter of the murine 27.44 gene. The vector also includes a heavy chain immunoglobulin enhancer and the human gammal constant region (CH). The VH region of 128.1 was isolated by polymerase chain reaction and cloned into plasmid pAH4274. This was achieved by digesting the plasmid and the product with EcoRV and NheI. The VH gene was inserted in frame with the human gammal CH region CH at the 3' end of the VH-J region by means of a NheI site. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, parkingons and alzheimers disease.
                                                                                                 Q43847 standard;
Q43847;
20-OCT-1993 (fir.
Plasmid pAH4807.
          Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807 transferrin; receptor; antibody; brain; capillary; paH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AIDS; stroke; epllepsy; monoclonal; disease; Alzheimers disease; SP2/0 cell; ss.
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                                                                                                                                                                                                                                                                  GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGAGGGTTACG
                                                                                                                                                                                                                                                                                  CAGAAGTTCAAGGGCCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATG
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Pred. No. 6.39e-160;
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and neurological
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Control of the sequences given in Q43846-48 represent the expression vectors copal4625, pAH4807 and pAH4808. These vectors represent the cloning control of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4 crespectively, with the variable region of the murine monoclonal control of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4 crespectively, with the variable region of the murine monoclonal control of the feavy chain (VH) is derived from a murine control of the murine monoclonal control of the passes and the sequences encoding CH1. CH2 and CH3 are derived from control of the sequences encoding CH2. CH3 and CH3 are derived from control of the gamma-1 of the chimeric light chain vector, pAG4611 (see also Q43845), were transfected into Sp2/0 colls and clones were isolated. Antibody analysis using biosynthe-control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-1 can into spatial control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimeras. No detectable control of the gamma-3 and gamma-4 chimera
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                                                                                                                                                                                                                                                                                                 Sequence
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24-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALKE-) ALKERMES INC
                                                             425
                                                                                                                                          365
                                                                                                                                                                                                                                    Match 73.9%;
Local Similarity 87.0%;
ggagagaaccttgagtggattggacgtattaatcctcacaatggtggtactgactacaac 2087
                                                                                                                                                           gtccagctgcaacagtctggacctgaactggtgaagcctggagcttcaatgaagatttcc 1967
                                                                               tgcaaggcttctggttactcattcactggctacaccatgaactgggtgaagcagagccat 2027
                                                           TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT
                                                                                                                                      GTGCAGCTGCAGGAGCTCAGGACCTGAGGTGGAAGCCTGGAGGTTCAATGAAGATATCC
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US-800458.
                                                                                                                                                                                                                  Conservative
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1848..2546
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5566..5864
/*tag= h
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/note= "Undefined
3672..4001
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6720..6744
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/note= "Undefined
3133..3177
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/note= "128.1 VH/human
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                                                                                                                                                                                                                                                                                               2292 A;
                                                                                                                                                                                                                                      Score 257; DB 7; I
Pred. No. 6.39e-160;
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                                                                                                                                                                                                                                                                                               2285 G;
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17-NOV-1994
                                                                                                                                                     the Ab heavy and light chain variable region-encoding CDNA isolated from hybridomas producing a mouse or rat monoclonal Ab reacting with the ganglioside GM2 respectively into an expression vector for use in animal cells which contains the human Ab heavy and light chain constant region-encoding cDNA. The expression vectors are introduced into animal cells and the transformant thus obtained is cultured for the prodn. of a chimeric human Ab reacting with the ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric human Abs will not cause anti-mouse Ig Ab prodn. in the patient's body but show a prolonged blood half-life, with a reduced frequency of adverse effects, so that it can be expected to be superior to mouse monoclonal Abs in the efficacy in the treatment of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody; expression vector; heavy; light; hypervariable region; CDR; constant region; hyperdoning; immunoglobulin; KM-796; KM-750; KM-603; cancer;
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07-SEP-1992; JP-238452
(KYOW) KYOWA HAKKO KO
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17-MAR-1994.
                                            heavy and light chain sequences are CDR regions for use in chimeric Abs
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                              Features Table.
                                                                             Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603 heavy and light chain sequences are given in Q45426-30.
                                                                                                                                    cancer, for instance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric human Ab expression vectors are constructed by inserting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroblastoma and glioma.
Disclosure; Page 107-108; 191pp;
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                                                                                                                                                                                                                                                                                                         Disclosure; Page 14; 18pp; Japanese.

The sequences given in Q28522-23 encode fragments which were used in the construction of an agent for the treating and prevention of hypercalcaemia. The agent contained a portion of the antihuman parathyroid hormone-related protein monoclonal antibody (antihuman PTHrP MAb). The MAb was used as the active component in the agent. The agent further comprises a rodent/human chimeric MAb which has a rodent variable region and a human constant region and recognises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treatment and preventive agent for hypercalcaemia - contg. one anti-human para-thyroid-hormone-related protein monoclonal antia a rodent or chimera monoclonal antibody, fused gene and cell
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Antihuman parathyroid hormone-related protein; monoclonal antibody; variable region; rodent/human chimeric MAb; constant region; PTHrP;
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15-MAY-1990; JP-124581.
(KANF ) KANEKA CORP.
WPI; 92-320987/39.
                                                                                                                                                                                                                                                                        Sequence
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Mismatches 48;
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Mismatches 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ry useful to detect tumour cells expressing GD2 and to target

ry therapeutic agents, e.g. toxins, to such cells

ps Disclosure; Page 11; 31pp; English.

CC The present sequence encodes a recombinant single chain peptide,

CC SF11-scFv. The peptide is an antibody construct comprising the variable

CC SF11-scFv. The peptide is an antibody construct comprising the variable

CC cregions of the heavy and light chains of an antibody against

CC distaloganglisside (GD2) as a single chain Fv fragment (scFv). GD2 occurs

CC in many tumours types including neuroblastoma, osteosarcomas and other

CC soft tissue sarcomas, medulloblastomas, high grade astrocytomas,

CC melanomas and small cell lung cancer. The peptide can be detectably

CC distaloganglisside (GD1) as a toxin, streptavidin or a pro-drug

CC GD2. It can also be used to target delivery of a therapeutic or

CC converting enzyme, to cells expressing GD2. The peptide may further

CC comprise CD8 to facilitate the formation of GD2-targeted lymphocytes.
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local :
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717 BP;
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Single chain anti-disialoganglioside GD2 antibody 5F11-scFv.
Antibody construct; disialoganglioside; GD2; single chain Fv fr.
scFv; tumour; neuroblastoma; osteosarcoma; soft tissue sarcoma;
tissue imaging; target delivery; toxin; streptavidin;
tissue imaging; converting enzyme; GD2-targeted lymphocyte; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant single chain anti-disialoganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheung NV, Guo H, Larson WPI; 97-479996/44.
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20-MAR-1996; US-013703.
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cagaagttcaagggcaaggccacattgactgtagacaagtcctccagcacagcctacatg
                                                                                        GACTGGTACTTCGATGTCTGGGGGCGCAGGGACCACGGTCAC
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larity 86.7%;
Conservative
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Pred. No. 3.10e-149;
0; Mismatches 43;
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The 15311 standard, DNA; 1175 BP.

AC 78631; 980 (first entry)

DT (0-APR-1998) (first entry)

DT (0-APR-1998) (first entry)

Single chain anti-disialoganglioside GD2 antibody SF11-scFv-streptavidin. Mantibody construct; disialoganglioside; GD2; single chain Fv fragment; KW scFv tumour, neuroblastoma; osteosarcoma; soft tissue sarcoma; kW stissue imaging; target delivery; toxin; streptavidin; KW pro-drug converting enzyme; GD2-targeted lymphocyte; ss.

Synthetic.

Location/Qualifiers

FT misc_feature 711.710

FT misc_feature 711.710

FT misc_feature 711.710

FT misc_feature 711.710

FT misc_feature 741.115 sF11*

FT misc_feature 741.117

Anote= "inker sequence"

FT misc_feature 741.173.3

PT 20-MAR-1997; U04427.

PR W0973434-A1

DS -SBF1997: U04427.

PR W097344-A1

DS -SBF1997: U04427.

PR W097349-A1

DS -SBF1997: U04427.

PR 20-MAR-1995; U04427.

PR 20-MAR-1
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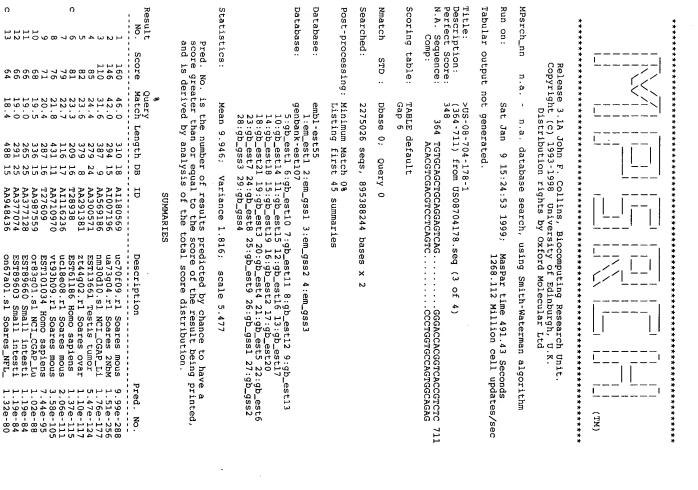
CC Disclosure; Page 12; 31pp; English.

CC The present sequence encodes a recombinant single chain peptide, comparising the variable regions of the heavy and light chains of an antibody against comparising comparisity through the heavy and light chains of an antibody against comparisity through the present including neuroblastoma, osteosarcomas and other comparisity through the present such as a single chain Fv fragment (scFv). GD2 occurs in many tumours types including neuroblastoma, osteosarcomas and other comparison medulloblastomas, high grade astrocytomas, comparison that tissue sarcovates and other comparison to target delivery of a therapeutic or comparison to target delivery of a therapeutic or comparison to target delivery of a therapeutic or peptide may further comparise CD8 to facilitate the formation of comparison c
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Pred. No. 3.10e-149;
0; Mismatches 43;
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ALIGNMENTS

FEATURES Source			TITLE JOURNAL COMMENT		REFERENCE		ORGANISM	SOURCE	NID	ACCESSION	DEFINITION	RESULT 1
Location/Qualifiers 1. 310 /organism="Mus musculus" /strain="C57BL/6J"	Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:915085 Seq primer: -28m13 rev2_ET from Amersham.	Contact: Marra M/Mouse EST Project	Waterston,R. The WashU-HHMI Mouse EST Project Unpublished (1996)	Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and	1 (bases 1 to 310)	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Mus musculus	house mouse.	g3731207	H*3101/3 SHIMITEL TO 9D:M13312 TO HEAVY CHAIN EXECUTIVE VI REGION (HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene mRNA, complete (MOUSE);, mRNA sequence. AT180569	uc70f09.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone	AT180569 310 bp mRNA EST 08-00T-1998

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on67a01.sl Soares_NFL_

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DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCCAACTGCAGCAGCCTGGGG-TAAGCTTGTGAAGCCTGG-GGTTCAGTGAAGCTGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCAAGACTTCTGGTTACTCACTCACTGGCCACCATGAACTGGGTGAAGCAGAGCCAT
                                                                                                                                                                                                                                                                                                                                                         g3216753
EST.
Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Lc Tel: 314 286 1800
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheri; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 294)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub; Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                             AI007196 294 bp mRNA EST 12-JUN-1998 ua73904.rl Soares 2NbMT Mus musculus cDNA clone 1363158 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                     The WashU-HHMI Mouse Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230;
                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                         house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.

RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="mammary
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="1431017"
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77 c 85 g
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79.3%;
                                                                                                                                       EST Project
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Pred. No. 9.99e-288;
0; Mismatches 58;
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                    Louis,
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ORIGIN

Matches

COMMENT

Tumor Gene Index

NID

ACCESSION

SOURCE KEYWORDS

REFERENCE

AUTHORS

RESULT LOCUS

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REFERENCE
AUTHORS
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Best Local :
       TITLE
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                                                                                                                                                                                                                                                                                                                 TCAAAAGTTCAAGGACAAGGCCACATTGACTGTAGACAAATTCACCAGCACAGCCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                             CTGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCA
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                                                                                                                                                                                                                                                                                                                                                                       TATACAAGGCATTGAATGGATTGGTAACATTGACCCTTCAGATAGTGGAACTCACTACAA 181
                                                                                                                                                                                                                                                                                                                                                         TGGAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
                                                                                                    g2342240
EST.
Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammal
Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 387)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                         AA569186 387 bp
nm30d10.s1 NCI_CGAP_
similar to gb:L02325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trace considered overall poor
Seg primer: -28ml3 rev2 ET fro
High quality sequence stop: 1.
                                                                                     numan.
                                                                                                                                 AA569186
                                                                                                                                           mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:896378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.0%;
larity 76.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
a 68 c 77 g
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/clone="1363158"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rounds of normalization,
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                                                                                                                                                     387 bp mRNA
NCI_CGAP_Lip2 Homo
gb:L02325 IG HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 146; DB 15; 1
Pred. No. 1.51e-256;
0; Mismatches 66;
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                                                                                                                                                        sapiens cDNA clone IMAGE:10
CHAIN PRECURSOR V-I REGION
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                                                           Mammalia;
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IMAGE:1061683
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                                                                                                                                                                                                                                                                                                                 GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
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                                                                                                                                                       AA300571
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Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                     g1953132
                                    Eukaryotae; mitochond;
Vertebrata; Mammalia;
                                                                             Homo sapiens
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                                                                                                                                                                                                                                       AA300571
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Seq primer: -40m13 fwd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             www-bio.llnl.gov/bbrp/image/image.html
                                                                                                  human.
(bases 1 to 279)
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Location/Qualifiers
1. .387
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/Organism="Homo sapiens"
/note="Vector: pANPI0; mRNA made from liposarcoma, cDNA
made by oligo-dT priming. Non- directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:1061683"
/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
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                                  mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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                                                                                                                                                                                                                                   279 bp
                                                                                                                                                                                        79 bp mRNA EST 18-APR-1997 tumor Homo sapiens cDNA 5' end similar to similar in mu heavy chain, VDJC regions (GB:M18812), mRNA
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Pred. No. 1.76e-177;
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                                                                                                   G
                                                                                                                                                                                                                                                                        GGACAAGGGCTTNAGTGGATGGGATGGATCAACCCTAAAAGTGGTGGCACAAACTATGCA 271
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zt44g02.rl Soares ovary 5' similar to gb:M18512 (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser.C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence based upon 83 million nucleotides of cDNA sequence 377 (6547 Suppl), 3-174 (1995)
                                                                            AA291381
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EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):192212"
/db_xref="taxon:9606"
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<1. .>279
74 c 85 g
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                                                                GAGCTGAGGAACCTGAGATCTGACGACACGGCCATATATTACTGTGCGAG 324
                                                                                                                                                                                            GGGAGTTTTCAGGACAGAGTCAGCTTGACCACTGACACCCCACGAATACAGCCTACATG
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                                                                                                                              CAGAAGTTCAAGGGCCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATG
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Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 361.
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| Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
| Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
| Parsons,J., Rifkin,L., Rohling,T., Tan,F., Trevaskis,E.,
| Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1576 Std Error: 0.00
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4444 Forest Park Parkway,
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Vertebrata; Mammalia;
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Similarity 65.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 314 286 1810
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/lab_host="DH10B (ampicillin
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.3%;
Best Local Similarity 71.7%;
Matches 134; Conservative
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                                                                                                                            135 CTAGTGAAGGTGTATCCAGAAGCCTTGCAGGAAACCTTCACTGAGGCCCCAGGCTTCTTC 194
                                                                                                                                                                                                                513
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Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,
Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weldman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Xim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of CDNA Sequence
                                                                                                    CCAGTGAATGAGTAACCAGAAGTCTTGCAGGATATCTTCATTGAACCTCCAGGCTTCACC
                                                                                                                                                                                                                                   ATCCATCCCATCCAAGCCTTTGTCCGGGGGCCTGGCGACCCAATGCATAGCATAG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T28938
g611036
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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Eukaryotae; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (tdbinfo@tdb.tigr.org)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tdbinfo@tdb.tigr.org
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387
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<1. .>209
1 62 c 48 g 5
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 81; DB 16; L
Pred. No. 1.37e-115;
0; Mismatches 53;
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JOURNAL
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                                                                                546
  606 AGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG
                                          62
                                                                                                                                                                 Local Similarity
nes 94; Consen
                                                                                                                      2 AGAAGTTCAAGAACAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGC 61
                                                                                AACTCAGCAGCCTGACATCTGAGGACACTGCGGTCTATTACTGTGGAAG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 116)

Marra,M., Hillier,L., Allen,M., Le,M., Martin,J., Morris,M., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ucl8e08.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone 1398374 5', similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN); gb:X67210 M.musculus rearranged immunoglobulin gamma 2b heavy (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
WashUrHHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g3516560
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314 286 1810
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                                                                                                                                                               22.7%;
larity 86.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                /tissue_type="mammary
/dev_stage="4 weeks"
/lab_host="DH10B"
32 c 25 g
                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="1398374"
/clone_lib="Soares mouse mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonaldo
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                                                                                                                                                                                                                                                                                                                                                   /sex="male"
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                                                                                                                                                             Score 79; DB 17; L
Pred. No. 2.06e-111;
0; Mismatches 15;
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                                                                                                                                                                                            124 AGTCTGGACCTGAAGAAGAAGCCTGGAGAGACAGTCAAGATCTCCTGCAAGGCTTCTG 183
                                                                                                                                               378 AGTCAGGACCTGAGGTGGAGCCTGGAGGTTCAATGAAGATATCCTGCAAGACTTCTG
                    244 AGTGGATGGGCTGGATAAACACCTACTCTGGAGTGCCAACATATGCTGATGACTTCAAGG 303
                                                              GTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAAAGAACCTTG
                                                                                                       GGTATACCTTCACAACCTATGGAATGAGCTGGGTGAAACAGGCTCCAGGAAAGGGTTTAA 243
vt93h09.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone 1178753 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:X70423 M.musculus mRNA for monoclonal antibody heavy chain gamma (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                 112
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                                                                                                                                                                                                                                       Conservative
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
103 c 112 g
                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="mammary gland"
/dev_stage="4 weeks"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="1178753"
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                                                                                                                                                                                                                                                         21.8%;
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                                                                                                                                                                                                                                                         Score 76; DB 11; L
Pred. No. 3.58e-105;
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Sarcopterygii; Choanata; Tetrapoda; Anniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarnhini; Hominidae; Homo.

Eutheria; Archonta; Primates; Catarnhini; Hominidae; Homo.

(CE 1 (bases 1 to 287)

RAdams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chlu, M.-W.,

Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,

Glodek, A., Genhm, C.L., Hanna, M.C., Hedblom, E., Hinkle JT, P.S.,

Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,

Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,

Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,

Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,

Weldman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,

Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,

Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,

Gruber, J.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,

Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns

Based Upon 52 Million Basepairs of CDNA Sequence
                         GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATATCC 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Resonant Chapter Rd, Gaithersburg, Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g609707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Venter, JC
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larity 70.3%;
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                                                                                                                                                                                       Score 71; DB 16;
Pred. No. 7.44e-95;
0; Mismatches 52
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urg, MD 20878
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365 GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGAGCCTGGAGGTTCAATGAAGATATCC 424
                                                                                                      92 TGCTTGGCCTCTGGAGGCACCTTCGGTAGTTCGACTGTCAGCTGGGTGCGACAGGCCCCT 151
                                                                                                                                                                                    32 GTCCAGATAGAACAGTCAGGGGCTGAGGTGAAGGCCAGGGTCTTCGGTGAAGGTCACC 91
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                                        GGACAACGGCCTGAGTGGATGGGGAAGATCATCCCCATCGCTCATTCAGCGAACTACGCA 211
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                                                                              TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT 484
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similar to
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Seg primer: 40ml3 fwd. ET from Amersham
High quality sequence stop: 322.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anat
Tumor Gene Index_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Ver
Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA987559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www-bio.linl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                            19.5%;
larity 61.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        /Organism="Homo sapiens"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
/clone="IMACE:1602480"
                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
86 c 100 g 68
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gb:M87789 IG
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                                                                                                                                                                                                                                                               Score 68; I
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Homo sapiens cDNA clone IMAGE:1602480
GAMMA-1 CHAIN C REGION (HUMAN);, mRNA
                                                                                                                                                                                                                                              Mismatches 111; Indels
                                                                                                                                                                                                                                                                                    DB 15;
                                                                                                                                                                                                                                                                 .02e-88
                                                                                                                                                                                                                                                                                  Length 336;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Woreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Zu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAG 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGAAGTTTCAGGACAGAATCACAATAACCGCGGGACAAATCTACGGCGTCAGTCTACATG
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EST.
                                                                                                                                                                                                                                                                                                                                                   Fax: 3018699423
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA377128 265 bp mRNA EST 21-APR-1997
EST899660 Small intestine I Homo sapiens cDNA 5' end similar to
similar to immunoglobulin heavy chain, VDJ region, mRNA sequence.
AA377128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other_ESTs: THC167579
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive, Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams,M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 265)
ms,M.D., Kerlavage,A.R., Fleischmann,R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute for Genomic Research
2 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                   57
           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 (6547 Suppl),
                                                                                                                                                                            note="Organ: small intestine; '
Site_1: EcoRI; Site_2: xhoI"
   /db_xref="RTCC (inhost):181546"
   /db_xref="taxon:9606"
   /clone_lib="Small intestine I"
                                                                                                                                                          /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                         ∕organism≃"Homo sapiens"
                             19.0%;
      Score 66; DB 25;
Pred. No. 1.19e-84;
0; Mismatches 49
                                                                                                                   79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-174 (1995)
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                                                                                                                                                                                                                                                                    intestine; Vector: pBluescript SK-;
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                                               Length 265;
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         Indels
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      Gaps
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      mRNA
BASE COUNT
ORIGIN
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AUTHORS
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 37
96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
AA377074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                               Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
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                           <1. .>291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblon, E., Hinkle, P.S. Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, F.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P. J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGGGCTCGAGTGGATGGGATGGATCACCGGTTACAATGGT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCATGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive, Tel: 3018699056
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                        Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Humani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
                                                                                                                                              /note="Organ: small intestine; Site_1: ECORI; Site_2: XhOI"
/db_xref="APCC (inhost):181500"
/db_xref="taxon:9606"
                                                                     /dev_stage="adult"
                                                                                                                   /clone_lib="Small
                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
89 g
                                                                                                                   intestine
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       61
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                                                                                                                                                                                                                                                             Vector: pBluescript SK-;
       1 others
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SOURCE
ORGANISM
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AUTHORS
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Best Local S
Matches 13
                           Query Match
Best Local :
        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 CAGAAGTTTCGGGGGAGAGTCAC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 GTGCAGCTGGTGCAATCTGGGGCTGAGGTGAAGGAGCCTGGGTCTTCTGTGAAAGTNTCG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCAT 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGACAGGGACTTGAGTGGATGGATGGATGAACCCAGCAAATGGAGGCTCCGACTGTGCA 254
18.4%;
1 Similarity 71.4%;
115; Conservati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY48436 488 bp mRNA EST 23-JUN-1998 on57a01.51 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1561704 3' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g3109689
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information. Insert Length: 1240 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 488)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 19.0%;
Similarity 66.0%;
134; Conservative
                                                                                                               108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (301) 496-1550
                                                                                                                                                                                                     /note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-303087, 682632-687239, 726408-728711, and 72996-733399. Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene Index
                                                                                                                              /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                       /clone-"IMAGE:1561704"
                                                                                                                                                                                        /db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 25; Lengua ....
Pred. No. 1.19e-84;
""" matches 69; Indels
    Score 64; DB 15;
Pred. No. 1.32e-80;
0; Mismatches 45
                                                                                                         88 g
      Mismatches 45;
                                                                                                           181 t
                                          Length 488;
      Indels
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                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                           FEATURES
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                                                                                                        Query Match 17.8%;
Best Local Similarity 72.8%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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                                                                                                                                                                                                                                                           mRNA
                                                                                                                                                                                                                                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 GTGTTACCATTGCCAGCATTGATCCACCCA-TCCACTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  594 GTGCTGGACGACTTGTCTACAGTAAATGTGGCCCTTGCCCCTTGAACTTCTGGTTGTAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 GTGCTCATGGACGTGTCCCTGGTTATGGTGACTCTGCCCTGGAACTTCTGTGCATATGTT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 CTCGCACAGTAATACACGGCCATGTCCTCAGATCTCAGGCTGCTCAGCTCCGTGTAGGCT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria: Archonta: Primates: Catarrifini: Hominidae: Homo.

Eutheria: Archonta: Primates: Catarrifini: Hominidae: Homo.

RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,

Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,

Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,

Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,

Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,

Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,

Weldman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,

Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,

Fischer, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H.,

Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,

Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,

Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns

Based Upon 52 Million Basepairs of CDNA Sequence
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GTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g611768
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Institute for Genomic Rese
932 Clopper Rd, Gaithersburg,
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T29670 238 bp mRNA ESCENT89669 Homo sapiens cDNA 5' end similar chain V region (GB:X61012) (HT:3230).
                                                                                                                                                                                                                                                                                                                                                                 Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR D: (tdbinfo@tdb.tigr.org).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                           /organism="Homo sapiens" <1. .>238
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 . 238
                                                                                                                                                                                                                                   .>238
70 c
                                                                                                     Score 62; DB 16; Le
Pred. No. 1.39e-76;
0; Mismatches 37;
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163 TGCAAGGCTTCTGGTTACACCTTTACCAGCTACGGTATCAGCTGGGTGCGACAGGCCCCT 222

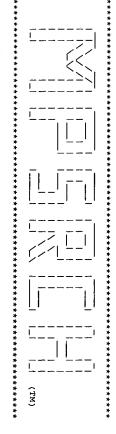
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TITLE
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Matches
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201 R-SYTCVRKYCVMWMTKKV--VKKYHVVBBGCHBTDSKCKTMWMTNKHVMTSTTD 252
                                                                                 141
                                                                                                                      631 GTCCTCAGATGTCAGACTGAGGAGCTCCATGTAGGCTGTGCTGGACGACTTGTCTACAGT 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 GGACAAGGGCTTGAGT 238
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                                                                                                                                                                                                 TSYBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYW 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CWBHYNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRAT 200
                                                                                                                                                          BVBNTKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMW 140
                                         AAATGTGGCCTTGCCCTTGAACTTCTGGTTGTAGTTAGTATCACCATTGTAAGGATTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. a
Suwon, Kyunggido, Korea
Tel: 82 331 290 0307
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 252) Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y. Large-Scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g2801165
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA clone 97SN1787, mRNA sequence. AA754459
                                                                                                                                                                                                                                                                                 h 17.0%;
Similarity 11.1%;
26; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SN1787"
                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                               Score 59; DB 12; Le
Pred. No. 1.35e-70;
120; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
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                                                                                                                                                                                                                                                                                   Indels
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511 AAGTCCAATCCACTCAAGGTTCTTTCCATGGCTCTGCTTCACCCAGTTCATGGTG 457

Search completed: Sat Jan 9 15:33:13 1999 Job time: 500 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Sat Jan 9 17:10:52 1999; MasPar time 100.47 Seconds 921.250 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-08-704-178-1 (322-363) from US08704178.seq (4 of 4) 42

322 AGGITCTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG 363
TCCAAGATGGAGACCAAGACCATTTAGAAGACTTCCATTTCC

Scoring table: TABLE default Gap 6

Nmatch STD: Dbase 0; Query 0

567134 seqs, 1101898692 bases x 2

Minimum Match 0% Listing first 45 summaries

Post-processing:

Database:

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl
13:em_ro 14:em_vi
genbank107

Database:

15:gb_bal 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov 21:gb_pat 22:gb_ph 23:gb_pl 24:gb_pl 25:gb_pr1 25:gb_pr1 25:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 30:gb_sts 31:gb_sy 32:gb_un 33:gb_vi

Statistics: Mean 7.713; Variance 4.202; scale 1.836

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 12 c 13	10 9 8	C 5 4 4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	Result No.
20	224	38 34 31 30	Score 42
47.6 47.6	57.1 57.1	90.5 81.0 81.0 73.8 71.4	Query Match 100.0
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23	3 2 2 3	21 28 28 21 21	DB 21
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Qy 322 AG RESULT 2 LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE	Query Ma Best Loo Matches	WORDS RCE RCANISM EERENCE UTHORS ITLE OURNAL TURES SOUICE E COUNT GIN	RESULT 1 LOCUS DEFINITION ACCESSION NID
AGGTTCTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG 363 2 S39590 Synthetic Recombinant Partial, 711 ntj. Synthetic Recombinant Partial, 711 ntj. 935990 9251113 . Mus sp.	100.0%; Score 42; DB 21; Similarity 100.0%; Pred. No. 3.22e-13; 42; Conservative 0; Mismatches 0	Unknown. Unknown. Unknown. Unclassified. 1 (bases 1 to 711) 1 (bases 1 to 711) 2 (bases 1 to 711) 3 (c. Richter, Kasprzyk, P.G. and Bird, R.E. Anti-erbB-2 antibodies, combinations thereof, and therapeutic and diagnostic uses thereof diagnostic uses thereof Location/Qualifiers 1. 711 /organism="unknown" 175 a 182 c 190 g 164 t	132406 711 bp DNA Sequence 1 from patent US 5587458. 132406 g1823197
3 363 3 363 SYN 10-FEB-1993 region [mice, Other	Length 711; ; Indels 0; Gaps 0;	of, and therapeutic an	T 07-JAN-1997

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1 (bases 1 to 720)

King, C. Richter, Kasprzyk, P.G. and Bird, R.E. Anti-erbB-2 antibodies, combinations thereo diagnostic uses thereof Patent: US 5587458 A 2 24-DEC-1996;
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KPWIYTTSNLASGVPARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGS
KLEIKGSTSGSGKSSEGKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQS
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/note="This sequence comes from Fig. 1."
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/db_xref="taxon:10095"
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354 AGGTTCTACCTCCGGCTCTGGGAAATCGTCTGAAGGTAAAGG
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Paul, S., Sun, M. and Gao, Q.-S.
Catalysis by natural and hybrid
Unpublished (1995)
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81.0%;
ilarity 90.5%;
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                                                                                                                                                                   /note="c-myc peptide-1; putative"
/function="facilitates recombinant
775. 792
                                                                                                   /note="poly-histidine; putative"
/function="facilitates recombinant
203 c 228 g 202 t
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LEWVATISGGDTYTYYPDSVKGRFTISRDNAKNNLFLQMSSLRSEDTALYFCGRGIAY
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/function="linkers
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/translation="DYIMTOTPLILSVTIGOPASISCKSSQSLLHTDGKTYLIWLLQR
/translation="DYIMTOTPLILSVTIGOPASISCKSSQSLLHTDGKTYLIWLLQR
PGQSSKRLLYLVSKLDSGVDDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPQT
PGGGTKLEIKRADAAPGSTSGSGKSSEGKGVKLVESGGGLVKFGGSLKLSCAASGFT
FSIYGMSWFFQTPEKRLEWYATISGDDTYTYYPDSVKGRFTISRDNAKNNLFLQMSSL
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translation qualifiers
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PGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPQT
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/product="antibody heavy chain"
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/product="antibody"
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antibody.
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L43544
 81.0%;
Similarity 90.5%;
38; Conservat'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paul, S., Sun, M. and Gao, Q.-S.
Catalysis by natural and hybrid single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Vertebrata; Eutheria; Rodentia; Sciurognathi; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative"
/function="linkers between
<397. .744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="antibody"
/db_xref="PID:9896294"
/db_xref="PID:9896294"
/translation="bytherogreptilsvrigopasisckssosilhhidgktyllwilor
/translation="bytherogreptilsvrigopasisckspoolitylycwogriffpQr
PGOSPKRLIYLVSKLDSGVPDRFTGSGSGSTDFTLKISRVEAEDLGVYYCWOGTHFPQT
PGOSPKLEIKADAAPGSTSGSGKSSECKGQVQLQESGPGLVAPSQSLSITCTVSGFS
LTGYGOVNWAPROPPGKGLEMLGMIWGDONTDYNSALKSRLSISKDNSKSOVFILKMNSH
LTGYGOVNWAPROPPGKGLEMLGMIWGDONTDYNSALKSRLSISKDNSKSOVFILKMNSH
LTGYGOVNWAPROPPGKGLEMLGMIWGDGTTVTVSSTKTTPPSVYPAAAHHHHHHGAAEQKLIS
                                                                                                                                                                                                                                                                                                                     <397. .>744
/note="This CDS feature is included to show the
/note="This CDS feature is included to show the
translation of the corresponding V_region. Presently
translation qualifiers on V_region features are illegal."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="PID:g896292"
/translation="DVLMTQTPLTLSVTIGQPASISCKSSQSLLHTDGKTYLIWLLQR
PGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal."
                                                                                                 /note="poly-histidine; putative"
/function="facilitates recombinant
217 c 217 g 190 t
                                                                                                                                                         /note="c-myc peptide-1; putative"
/function="facilitates recombinant
784. 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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LDYWGQGTTVTVSS "
                                                                                                                                                                                                                                                                                                                                                                                             /product="antibody heavy chain"
<397. .>744
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                     /db_xref="PID:9896293"
/translation="QVQLQESGPGLYAPSQSLSITCTVSGFSLTGYGVNWVRQPPGKG
                                                                                                                                                                                                                                                                                                               codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative"
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Score 34; DB 28;
Pred. No. 5.00e-08;
0; Mismatches 4
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132413
g1823204
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I32414
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1 (bases 1 to 47)

King, C. Richter, Kasprzyk, P.G. and Bird, R.E. Anti-erbB-2 antibodies, combinations thereodiagnostic uses thereof

Patent: US 587458-A 9 24-DEC-1996;
g310725
IgM-binding protein;
monoclonal antibody.
                                      SYNBETZX 717 bp mRNA
Synthetic single-chain Fv fusion protein (Bet 2/212) mRNA,
constructed from variable light and heavy chain regions of rat
monoclonal antibody Bet 2, 3 end of cds.
                                                                                                                                                                                                                                                     King, C.Richter, Kasprzyk, P.G. and Bir
Anti-rbB-2 antibodies, combinations
diagnostic uses thereof
Patent: US 5587458-A 8 24-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g1823205
                                                                                                                                                                                                                                                                                                                     Unknown
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                                                                                                                                                         h 71.4%;
Similarity 100.0%;
30; Conservative
                                                                                                                                                                                                                                                                                                           Unclassified
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Similarity 100.0%;
31; Conservative
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1 7 c 16 g
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1. .47
                                                                                                                                                                                                            /organism="unknown"
9 c 10 g
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patent US 5587458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 21;
Pred. No. 3.74e-06;
0; Mismatches 0
                                                                                                                                                         Score 30; DB 21;
Pred. No. 1.54e-05;
0; Mismatches 0
         fusion
         protein;
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                                                                                                                                                                                                                                                                                     Bird, R.E.
         fusion
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9207841/212 SCA protein; fusion protein; fusion protein; fusion protein; fusion protein; fusion protein; fusion protein protein; fusion protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
                                                                                                                                                                                                                                                                                                                                                     Gibbs,R.A., Posner,B.A., Filpula,D.R., Dodd,S.W., Finkelman,M.A. J., Lee,T.K., Wroble,M., Whitlow,M. and Benkovic,S.J. Construction and characterization of a single-chain catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYN7A41 743 bp DNA SYN 04-MAR-1993 Synthetic single-chain antigen-binding protein gene (7A4-1/212 SCA) constructed from the antigen-binding (Fab) fragment of mouse catalytic monoclonal antibody NPN43C9 and linker DNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 artificial sequence.

1 (bases 1 to 717)

Lee, T.K., Rollence, M.L., Hallberg, P.L., Oelkuct, M.S., Dodd, S.W.,

Nagle, J.W. and Filpula, D.R.

Production of engineered igM-binding single-chain antibodies in
                                                                                                                                                                                                                                                                                                                          antibody
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larity 78.6%;
Conservative
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                              /gene≐"7A4-1/212"
<1. .735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="variable heavy chain derived antibody Bet 2 (ATCC HB88)" a 170 c 186 g 168 t
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antibody Bet 2 (ATCC HB88)"
313. .354
                                                                                                                                                           /organism="artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="DVTQSFSLLSASVGDRVTLSCKGSQNIVNYLAWYQQKLGEAPKL
LIFNTNSLQTGIPSRESGSGSGTDYTLTISGLQPEDVATYFCYQYKNGYTFGAGTKLE
LKGSTSGSGKSSEGKGEVQLVESGGGLVQPGSSLKVSCVASRFTFSSYVMHWFRQAPE
NGIEWLAYINTDSSSAHYAETVKGRFTISRDNAKNTVDMQLSSLRSEDTAMYFCARGG
/gene="7A4-1/212"
                                                                                                                      /db_xref="taxon:29278"
                                                                                                                                                                                                                     Location/Qualifiers
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/product="fusion protein"
/db_xref="PID:g310726"
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/db_xref="taxon:29278"
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                                                                                                                                                                                                                                                                                                                                                  characterization of a single-chain catalytic
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Pred. No.
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protein.
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IgM-binding protein; fusion protein; fusion monocional antibody.
Artificial gene cDNA to mRNA.
artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNDA4AX 744 bp mRNA SYN 01-MAR-1996 Synthetic single-chain Fv fusion protein (DA4.4/212) mRNA, constructed from variable light and heavy chain regions of mountain mathematical constructions of mountain constructions.
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1 (bases 1 to 744)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagle, J.W. and Filpula, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 57.1%;
Similarity 78.6%;
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lee, T.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           _Microbiol. 14 (5), 371-376 (1995)
                                                                                                                              /transl_table=11
/function="binds human IgM"
/function="binds human IgM"
/product="fusion protein"
/db_xref="piD:g310740"
/translation="buvnTQSPSSLANSVGQKVTMSCKSSQSLLNSSNQKNYLAWYQQKTABASTATIONSTATESGVPDFTIGSGSGTDFTLTISSVQAEDLADYFCQQHYSTPF
TFGSGTKLEIKGSTSGSGKSSEGKGQVQLQQPGAEFVKPGAPVKLSCKASGYPFTTYW
VNMMKQRPGRGLEWIGRIDPTDSETLXNQKFKDKATLTVDKSSSTAYIQLSSLTSEDS
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a 176 c
/note="linker segment" 382. .744
                                                        /note="variable light chain antibody DA4.4 (ATCC HB57)"
                                                                                                                    AVYYCARETYDYPFAYWGQGTLVTVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="7A4-1/212"
/note="synthetic linker"
382. .735
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/transl=17A4-1/212 SCA fusion protein"
/product="7A4-1/212 SCA fusion protein"
/db_xref="PID:9207840"
/translation="DVVMTOTPSSLAMSVGQKVTMSCKSSGSLLNISNQKNYLAWYQQ
KPGQSPKLLVYFASTRESGYDERFICSGSGTDFTLTISSVQAEDQADYFCQQHYRAPR
TFGGGTKLEIKGSTSGSGKSSEGKGQVQLVESGPGLVAPSQSLSITCTVSGISLSRYN
VHWVRQSPGKKLEWLGMIWGGGSIEYNPALKSRLSISKDNSKSQIFLKMNSLQTDDSA
                                                                                                                                                                                                                                                                                                                                                        /organism="artificial
/db_xref="taxon:29278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rollence, M.L.,
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                                                                                                                                                                                                                                                                                                                     /standard_name="DA4.4/212 sFv protein"
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                                                                            derived from mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chloroplast Hordeum vulgare
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnollop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liliopsida: Poales; Poaceae; Hordeum.

1 (bases 1 to 228)
Martin,M., Casano,L.M. and Sabater,B.
Identification of the product of ndhA gene as a thylakoid protein synthesized in response to photooxidative treatment Plant Cell Physiol. 37 (3), 293-298 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast,
S82816
Chloroplast Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry [NCBI gibbsq 179114] from This sequence comes from Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ndha=NDH-A [Hordeum vulgare=barley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             barley cv. Hassan leaf extracts
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                        NDH-A protein; ndhA gene.
                                                    Y13729
                                                             Hordeum vulgare
                                                                            HVNDHA590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenBank staff at the National Library of Medicine created this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
33; Conser
              Hordeum vulgare.
                                                                                                                                                                                Similarity
22; Conser
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a 187 c
                                                                                                                                                                                                                                          /db_xref="PID:g1754725"
/translation="PFDLPEAGELVAGYQTEYSGIKYGLFYLVSYLNLLVSSLFVTV
LYLGGWNFSIPYISFEDFOMNKAVGILEMTM"
15 c 38 g 92 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="variable heavy chain derived from mouse monoclonal
antibody DA4.4 (ATCC HB57)"
187 c 186 g 179 t
                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                              'product="NDH-A"
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78.6%;
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                                                             590 bp DNA
ce chloroplast
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Pred.
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No. 5.35e-02;
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                                                              DNA for ndhA gene 3'end (exons 1 & 2).
                                                                                                                                                                                            8.14e+00;
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153 GATTTACCAGAAGCAGAGGAAGAA 176
                                                                                                                                                                                                                                                                                                                                                                                                            348 GATTTACCAGAACCAGAGGTAGAA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity hes 22; Conser
                                                                                                                Hordeum vulgare.
Chloroplast Hordeum vulgare
Enkaryota; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta;
Magnollophyta; Liliopsida; Poales; Poaceae; Hordeum.

1 (bases 1 to 1636)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcript editing in several gram. Plant Physiol. 115, 313-313 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-JUN-1997) Sabater B., Biologia Vegetal, Fac.
Ciencias, Campus Universitario, Universidad de Alcala de Henares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sabater, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; vascular plants; seed plants; Magnoliophyta Liliopsida; Poales; Poaceae; Hordeum.
                                                                                                                                                                                                                                            NADH dehydrogenase; ndhA gene; subunit
                                                                                                                                                                                                                                                                                    Hordeum vulgare
AJ010977
                                                                                                                                                                                                                                                                                                                             HVU010977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of ndhA gene of barley (Hordeum vulgare L.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lopez,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cra. Madrid-Barcelona km 33,6, Alcala de Henares. Madrid 28871
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                                        Nucleic Acids
                                                                            Precise branch point mapping
                                                                                                    Vogel,J.,
                                                           intermediates
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(bases 1 to 1636)
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ilarity 91.7%;
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/note="C to U
532
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/translation="SNSSSTVDIVEAQSKYGFFGWNIWRQPIGFLVFLISSLAECERL
PFDLPEAEEELVAGYQTEYSGIKYGLFYLVSYLNLLVSSLFVTVLYLGGWNFSIPYIS
FFDFFQMNKAVGILEMTMGIFITLTKAYLFLFISITIRWTLPRMRMDQLLNLGWKFLL
PISLGNLLLTTSSQLVSL"
                                                                                                 Hess, W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ndhA"
/note="C to U RNA editing"
1 89 c 92 g 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="NDH-A protein"
/db_xref="PID:e321930"
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                                                                                                                                                                                                                                                                                                     1636 bp DNA
                                        Res. 25
                                                                                                    and Borner, T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20; DB 23;
Pred. No. 8.14e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATTTACCAGAACCAGAGGTAGAA 325
                                             Kremsdorf,D., Favre,M., Jablonska,S., Obalek,S., Rueda,L.A., Lutzner,M.A., Blanchet-Bardon,C., Van Voorst Vader,P.C. and Orth,G. Molecular cloning and characterization of the genomes of nine newly recognized human papillomavirus types associated with epidermodysplasia verruciformis
J. Virol. 52 (3), 1013-1018 (1984)
85033930
3 (bases 1 to 7368)
                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus type 22.
Human papillomavirus type 22
Viruses; dsDNA viruses, no RNA stage;
Papillomavirus.
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  Farmer, A.D.
Direct Submission
                                                                                                                                                                                                                                                           Sequenced by Hajo Delius, Deutsches Krebsforschungzentrum, Angewandte Tumorvirologie, I.N.F. 506, W-6900 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                               g1020178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vogel,J
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Unpublished
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                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPU31780
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                                          (bases 1 to 7368)
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1366...>1636
/gene="ndha"
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/chloroplast
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1290. .1323
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91.7%;
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Pred. No. 8.14e+00;
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HPV22 was originally isolated from macules on the chest of an Italian epidermodysplasia verruciformis (EV) patient [2]. The HPV22 genome, like that of HPV9 9, 15, 17a/b, 23, 37, 38, is smaller than most PV genomes at approximately 7.4 kb. Phylogenetic reconstructions based on DNA sequences of established types indicate that HPV22 is most closely related to HPVs 23 and 38, and then to 15, 17, 37 and 9. Although Kremsdorf et al [2] found substantial cross-hybridization between HPV22 and HPV19, nucleotide sequence comparison fails to support a close relationship between these two topes.
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NISPGHKSKRLFVEHDSGLECSLNBAEDLTEEVEVPASAPAPAPAQGCYGSGHYTSLL
RCNNVKAVLLGKFKDAFGVSYNGLTROFESNHTCCKHWVLAIYAAKDBLIDASKQLLQ
QHCTYLMLQTFSPMSLYLCCFNVGKSRETVMRLLSSMLQVNENHILSEPPKIRSMIAA
LFWYKGSMNPAVYAFGBYPEMIMTQTMJHHQTADSVQFDLSEMIQWAYDQDYVDECTI
AYQYARLADSMSNARAFLAHNSQAKYVRECAQMYRYYKREENBOMSISAMHHGISKI
EGDGHWQDIVKFLRYQGLNFIVFLDKFRTFLKNFPKKNCLLICGPPDTGKSMFSMSIAM
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932. .2758
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/translation="MIGKQAFICDIVLEELVLPIDLHCHEELPELPEELEESVVEEEP
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VDLLLFCRFEIEQEEQRPVGQIYMRCQYCLKSLDLLEKLDICCSNQPFHKVRDHWKGRCRH
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                  /translation="MEKLSERFSALQEKLMDLYESGVEDLETQIQHWKLLRQEQVLFY
YARRHGILRLGYQPVPTLATSESKAKDAIAMGLLLESLQKSQYAEEPWTLVETSLETV
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                                                                                                                                                                                                                                                                               KALRGQVVSFANSKSHFWLQPLADAKLALLDDATEVCWQYIDAFLRNGLDGNMVSLDM
KHRAPCQMKFPPLIITSNISLKKEKKFPYLHSRIYEFEFPNKFPFDANDTPLFKLTDQ
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643. .945
                                                                               /product="regulatory protein
/db_xref="PID:g1020182"
                                                                                                                                                                                                                                                             SWASFFKRLWTQLELSDQEEEGENGETQRTFQCTTREVNGLI"
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note="cloned HPV-22 was obtained from the
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DVSLDIVNEICKYPDFLIMSNDVYGDSCFFCARREQCYARHNFYRGGLYGDAIPDDAV
QQDHKYYLPAASQTALENGYYFPTVSGSLVTSDAQLFNRPFWLKRAGGHNIGILIMND
MFYTVADNTRNTNFSISVASDGTTVNYDAKKIREFMRHVEEYQLSFILQLCRIPLEAE
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CKGLEIGRGQPLGYGTTGHPLFNKLHDTENPTERQEGTSDDRRNVSFDPKQVQMFIIG
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GRATRRSLSRESAESPRRGGRGGGGLTRSRSRSRSRTRESVDGGGVAPDEVGATLRS
IGRQHSGRLAQLLDAAKDPPVILLRGAANTLKCYRYRFRKKHAGSFQFISTTWSWVGG
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PSITVPQFESPRETIVYIQDIEGNTVVYPKYEERPTIILPTPSGPAIIQSPTHSSFDY
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KPDQGPEAPSSGEGGPPDDPSPENPQNPPGGEGEVEGAPSPGPAQGRDPVHESLLTGV
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/db_xref="PID:g1020184"
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                                    Chlamydiales; Chlamydiaceae; Chlamydia
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33 of 87 of the complete genome.
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2 (bases 1 to 13316)
Stephens, R.S., Kalman, S., Lammel, C.J.,
Aravind, L., Mitchell, W.P., Olinger, L.,
Koonin, E.V. and Davis, R.W.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-MAY-1998) Program of California, 235 Warren Hall, Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stephens, R.S., Kalman, S., Lammel, C.J., Fan, J., Marathe, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIQEGETNLNHVEQLSFQLQLNPDGSVAVDTSGNPIKHPFIPGESV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in Infectious Diseases, University Berkeley, CA 94720-7360, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fan, J., Marathe, R., Tatusov, R.L., Zhao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pathogen of Humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao,Q.,
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gene

CDS

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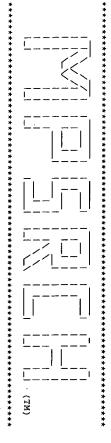
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331 CTCTGGTTCTGGTAAATCTTCT
                                                                                            h 47.6%;
Similarity 95.5%;
21; Conservative
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a 3167
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                                                                                                                                                                                                               3890
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Search completed: Sat Jan Job time: 107 secs. φ 17:12:39 1999 Qy

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat Jan 9 17:20:30 1999; MasPar time 20.09 Seconds 284.402 Million cell upda updates/sec

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363

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Post-processing: Minimum Match 0% Listing first 45 summaries

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14:part14 15:part15 16:part16 17:part7 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 5.992; Variance 4.139; scale 1.448

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Score	Query Match	Length DB	DB	Ĭ	Description	Pred. No.
<u>سر</u>	42	100.0	711	9	Q55180	Sequence encoding the	4.08e-12
2	42	100.0	711	18	T17728	Anti-erbB2 scFv cDNA.	4.08e-12
ω	42	100.0	711	29	T65006	Single-chain anti-erb	4.08e-12
4	42	100.0	761	7	Q43289	Sequence encoding a 4	4.08e-12
Ç,	42	100.0	803	ω	Q14831	Qm212 single chain an	4.08e-12
o	38	90.5	720	29	T65007	Single-chain anti-erb	6.29e-10
7	38	90.5	720	9	Q55181	Sequence encoding the	6.29e-10
œ	38	90.5	731	7	Q43287	Sequence encoding a m	6.29e-10
9	38	90.5	770	7	Q43290	Sequence encoding a 4	6.29e-10
c 10	32	76.2	91	9	Q51746	Oligonucleotide probe	1.03e-06
11	28	66.7	744	7	Q43288	Sequence encoding a m	1.24e-04
12	25	59.5	91	9	Q51746	Oligonucleotide probe	4.10e-03
13	24	57.1	797	22	T29058	CC49/212 SCA PLAP DNA	1.29e-02

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18 18 17 17 17	1888 1888 1888	20 20 20 20 20 20 20 20 20	24 23 21 21 20 20
		47.6 47.6 47.6 47.6 47.6 47.6 47.6 45.2	
134525 563 668 3537	33 1144 1144 2956 3279 3279	725 5600 5600 5600 5600 5600 5600 5362 9202	803 1460 738 738 738 39 47 47 66 36
		111 7 6 6 39 39 39	
1.84545 105868 004525 006496 006496	Q46603 Q44800 T99264 T99140 Q50946 Q51556	Q66840 Q43292 Q23963 Q62663 Q62663 Q38266 Q38251 Q38251 Q31678 Q31678 Q31678 Q31678 Q31678	T29059 Q43291 Q43293 Q643293 Q66841 Q51787 T86394 Q49187 Q49187 Q111195
Human Sterold recepto Chicken leucocytozoan Total base sequence o Sequence in a recombi IFN-alpha 61 gene and Sequence encoding B.t	oligonuc single single PUR-alph cy ength cy encodice enco	VL/ 217 ce encodi ce pHC pHC plasmid S-33-BCD S-33-BCD 1 - recom S-33-BCD 1 - recom S-33-BCD 1 - recom Additiona additiona	PLAP CC49/212 SCA DNA Sequence encoding div Sequence encoding sin CC49 VL / 217 / 4-4-2 Mixed oligonucleotide Sp6 anti-TNP antibody scFVR construction pr Ballast Constituent c Primer used in immuno
9.18e+00 9.18e+00 9.18e+00 2.57e+01 2.57e+01 2.57e+01			1.29e-02 1.29e-02 4.00e-02 4.00e-02 3.70e-01 3.70e-01 3.70e-01 1.10e+00

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Query M Best Lo Matches	Sequence	anim	grow	doma	erbB	23 a	The	Exam	qp185	rrea 2 mo	P-PSDB; R45442.	WPI;	Kasprzyk PG,	(MOL	30-JUN-1992;	21-0	06-JAN-1994.	₹094		cds	Key	Synthetic.	nono	sing	Sequ	21-JUL-1994	Q55180;	Q55180
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ilar Co	711 i	en a	sanc	domain of gp185	s no	2551	of h	a 7;	!	r ma 1 an	442.	WPI; 94-025878/03.	` ×	ECUL	; US		•	•					anti	n an	codi	æ		dard
Query Match 100.0%; Best Local Similarity 100.0%; Matches 42; Conservative	BP;	animals given a combination of	growing tumours were used in a	ert	engineered to express the erbB-2). Abs no. 21 and 23	F/08	uman	37p	į	tibo		03.		(MOLE-) MOLECULAR ONCOLOGY	US-906555	U08545			*t	<u>'</u>	F _O C		monoclonal antibody; ss.	ti-e	ng t	(first entry)		standard; cDNA; 711
100 100 vat	BP; days.	bina	e us	B-2	anc	4544	er	ĕ		dies			CR;	NCOI	555	•			*tag=	1171	Location/Qualifiers		-: SS	rbB1	he s	ent		ŇA;
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	Η,	the 2 Abs, tumours completely	trial of the efficacy of the Abs.	erbB-2. Nude mice manipulated to produce rapidly	engineered to express the numan erbs-z protein on its surface (N/ erbB-2). Abs no. 21 and 23 are directed against the extracellular	Ë	The source of human erbB-2 protein for the prodn. of antibodies		Č	Treatment of mailgnancies over-expressing ERB-[z - using at I														Single chain anti-erbB1 antibody; cancer therapy; prevention;	Вb			
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibition of proliferation or survival of, esp. malignant erbB2, reells - by introducing nucleic acid mol. encoding antibody homologue which is expressed and binds, pref. erbB2, protein intracellularly claim 42; Page 29-30; 48pp; English.

A nucleic acid comprises a first sequence encoding a signal peptide (R94019) linked to a second sequence (T17728) encoding a single chain Fv fragment (R94020) that binds a human erbB2 oncoprotein. The anti-erbB2 sFv portion is obtained by PCR using e23scFv plasmid as template. The signal peptide directs the scFv to the endoplasmic reticulum. The nucleic acid is incorporated into a plasmid or viral vector to facilitate expression of the scFv antibody expression of the homologue within e.g. an epithelial carcinoma cell. Intracellular expression of the homologue inhibits surface expression of erbB2 and thereby inhibits cell proliferation and cell survival and decreases
                                 US5587458-A.
24-DEC-1996.
07-OCT-1991; 772270.
07-OCT-1991; US-772270.
30-JUN-1992; US-906555.
2 14-MAY-1993; US-061092.
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Best Local
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23-AUG-1995; U10740.
06-SEP-1994; US-301339.
06-JUN-1995; US-468252.
(UABR-) UAB RES FOUND.
CUITIEL DT, Deshane J;
            Bird RE,
WPI; 97-(
                                                                                                                                                                                                                                      05-JUN-1997 (first entry)
Single-chain anti-erbB2 antibody e23(Fv) cDNA.
Single chain antibody; variable region; light chain; heavy breast cancer; ovarian cancer; non-small cell lung carcinom
                                                                                                                                                                                                                                                                                      T65006 standard; cDNA;
T65006;
05-JUN-1997 (first ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uncoprotein; erbB2; cell proliferation; tumour; cancer;
intracellular antibody homologue; single chain antibody; scFv;
gene therapy; ds.
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Anti-erbB2 scFv cDNA.
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                                                                                                                                                                                                                                immunodiagnosis;
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Local Similarity 100.0%;
les 42; Conservative
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         RE, Kasprzyk PG,
97-064831/06.
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                        King CR;
                                                                                                                                          e23(Fv)
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                                                                                                                                                                                                                           er; non-small cell lung carcinoma; cytotoxic agent; erbB-2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 18;
Pred. No. 4.08e-12;
0; Mismatches 0
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The present cDNA sequence codes for a calined single-chain antibody, cdesignated e23(FV), which binds to erbB-2. Monoclonal antibody e23 was generated by immunising mice with N/erbB-2 cells overexpressing the gpl85 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light- chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbB-2 gpl85 marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours. Sequence 711 BP; 175 A; 182 C; 189 G; 164 T;
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Best Local
                                                                                                                                                                       New multivalent antigen-binding protein e.g. contg. CC49) regions - useful in diagnosis, for destroying blood clots targetting cytotoxic agents or enzymes to tumour cells Example; Fig 15A; 118pp; English.

Free cysteines were engineered into the C-terminal of the 4-4-20/212 single-chain antigen-binding protein, in order chemically crosslink the protein. The design was based on hinge region found in antibodies between the CH1 and CH2 in the control of t
                                In order to try to reduce antigenicity in humans, the him sequence of the most common 1gG class, 1gGl, was chosen design for the hinge region, the C-terminal serine in the 4-4-20/212 singl-chain antigen-binding protein was made the serious control of the himself of the serious control of the serio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood JF;
WPI; 93-196999/24.
P-PSDB; R37647.
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Sequence encoding a 4-4-20/212 single-chain antigen-binding
protein with a single cysteine hinge.
Antibody; multivalent; variable region; heavy chain; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUN-1993.
20-NOV-1992; U09965.
25-NOV-1991; US-796936.
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27-SEP-1993
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Q43289 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ENZO-) ENZON INC.
Bird RE, Filpula
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Similarity 100.0%;
42; Conservative
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gen-binding protein was made the first second residue of the hinge was changed
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Pred. No. 4.08e-12;
0; Mismatches 0;
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Best Local :
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09116912-A.
14-NOV-1991;
07-MAY-1991; U03149.
08-MAY-1990; US-521258.
18-JUN-1990; US-539980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q14831;
17-FEB-1992 (first entry)
Qm212 single chain antigen binding protein with metal binding site.
Antigen binding; metal cations; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 73pp; English.

Disclosure; Fig 1; 73pp; English.

The sequence encodes Qm212, a single chain antigen binding protein having a metal binding site which is derived from the 4-4-20/212 protein (Bird et al., Science, 242:423-426 [1988]), Qm212 differs from 4-4-20/212 by amino acid substitutions at residue positions 60, 62, 115 and 117 to provide for contact amino acid residues, where three of these contact residues form a metal binding site. The organism form which the gene originated is not given in the specification. The protein may be used to selectively partition and/or remove metal cations from fluids. Preselected antigens can be used to remove metal protein complexes from a liquid phase or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from a cysteine to a serine. The hinge regions were added by introduction of a BstE II restriction site in the 3'-terminus of the gene encoding the 4-4-20/212 single-chain antigen-bind
                                                                           Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q14831
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mat_peptide
                                                 Synthetic.
                                                                                                                         breast cancer;
                                                                                                                                                   Single chain
                                                                                                                                                                     05-JUN-1997
Single-chain
                                                                                                                                                                                                                         T65007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   indicators of metal complex formation. The metal-protein complexes can also be used to promote a predetermined chemical reaction, e.g. hydrolysis of a peptide bond.

Sequence 803 BP; 224 A; 175 C; 197 G; 207 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New metal binding proteins - immunoglobulin and 3 contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; R15055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SCRI-) SCRIPPS CLINIC & RE.
Lerner RA, Roberts VN, Getzoff ED,
WPI; 91-353518/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                  immunodiagnosis;
                                                                                                                                                                                                                                              T65007 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399
                                                                                                                                                                                                                                                                                                                                                   322
                                                                           musculus.
                                                                                                                                                                                                                                                                                                                                                   AGGTTCTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG
                                                                                                                                                                                                                                                                                                                                                                             aggttctacctctggttctggtaaatcttctgaaggtaaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
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Similarity 100.0%;
                                                                                                          anti-erbB2 antibody e21(Fv) cDNA.
antibody; variable region; light chain; heavy charithous cancer; non-small cell lung carcinoma;
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
Location/Qualifiers
1..720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                               treatment;
                                                                                                                                                                                                                                                 cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 7; 1
Pred. No. 4.08e-12
                                                                                               cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 3; ]
Pred. No. 4.08e-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising aminoacid r
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tainer
                                                                                                  agent; erbB-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Benkovic
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                   363
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ll binding
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                                                                                                                                                   chain;
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PPI NESULATION OF STREET STREE
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Best Local :
       Query Match
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24-DEC-1996.
07-OCT-1991; 772270.
07-OCT-1991; US-772270.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 9; Columns 27-30; 28pp; English.

The present cDNA sequence codes for a claimed single-chain antibody e21 designated e21(FV), which binds to erbB-2. Monoclonal antibody e21 was generated by immunising mice with N/erbB-2 cells overexpressing the gpl85 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light- chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbB-2 gpl85 markers of breat extrapolations and the code of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q55181 :
Q55181;
                                                                                           The source of human erbB-2 protein for the prodn. of antibodies no. 33 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/373 cell 23 and 21 (Apress the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. Ir animals given a combination of the 2 Abs, tumours completely regressed after 11 days.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JAN-1-37%.
21-OCT-1992; U08545.
30-JUN-1992; US-906555.
(MOLE-) MOLECULAR ONCOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ARON-) ARONEX PHARM INC. Bird RE, Kasprzyk PG, King WPI; 97-064831/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours. Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells expressing this protein Example 9; Columns 27-30; 28pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single chain antibodies specific labels or cytotoxin, useful for c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; W15186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monoclonal antibody; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoding the single chain anti-erbB2 antibody, Ab no Single chain anti-erbB1 antibody; cancer therapy; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Treatment of malignancies over-expressing ERB-[2 - using at least 2 monoclonal antibodies which recognise different epitopes on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kasprzyk PG, King
WPI; 94-025878/03.
                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 8; 37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; R45443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9400136-A.
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1..171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.5%;
95.2%;
       90.5%;
                                                                                                                                                                                                                                                                                                                                                                               English
                                                                          184
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   Score
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Pred. No. 6.29e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain anti-erbB2 antibody, Ab no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection
                                                                      178
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n and treatme
       9
                                                                          179
Length 720
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                                                                      179 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gp185
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(ENZO-) ENZON INC.
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Antibody; multivalent; variable region.
                                                                                                               Antibody;
linker; so
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Example; Fig 10A; 118pp; English.

"4-4-20 VL" means the variable region of the light chain of the
4-4-20 mouse monoclonal antibody (Bird, R.E. et al., Science 242:423
(1988)). The number "212" refers to a specific 14-residue
polypeptide linker that links the 4-4-20 VL and the CC49 VH. See
Bedzyk, W.D. et al., J. Biol. Chem. 265:18615-18620 (1990). "CC49 VH"
is the variable region of the heavy chain of the CC49 antibody,
which binds to the TAG-72 antigen.
Sequence 731 BP; 190 A; 176 C; 180 G; 185 T;
                                                                                                                     27-SEP-1993 (first entry)
27-SEP-1993 (first entry)
Sequence encoding a 4-4-20/212 single-chain antigen-binding protein with the two cysteine hinge.
Antibody; multivalent; variable region; heavy chain; light
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20-NOV-1992; U09965.
25-NOV-1991; US-796936.
(ENZO-) ENZON INC.
                                                                                                                                                                                                                                                                                                                                 Q51746;
Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In order to try to reduce antigenicity in humans, the hinge sequence of the most common IgG class, IgG1, was chosen. In the design for the hinge region, the C-terminal serine in the 4-4-20/212 singl-chain antigen-binding protein was made the first serine of the hinge and the second residue of the hinge was change from a cysteine to a serine. The hinge regions were added by introduction of a BstE II restriction site in the 3'-terminus of the gene encoding the 4-4-20/212 single-chain antigen-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New multivalent antigen-binding protein e.g. contg. CC49 Mab regions - useful in diagnosis, for destroying blood clots and targetting cytotoxic agents or enzymes to tumour cells example; Fig 15B; 118pp; English.

Erree cysteines were engineered into the C-terminal of the Free cysteines were engineered into the C-terminal of the 4-4-20/212 single-chain antigen-binding protein, in order to chemically crosslink the protein. The design was based on the hinge region found in antibodies between the CH1 and CH2 regions.
                                                                             claim 3;
                                                                                                        (BECT ) BECTON DICKINSON CO. Shank D, Spears PA; WPI; 93-378844/48.
New ollgo:nucleotide probes detection and amplification
                                                                                                                                                                                       EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651
                                                                                                                                                                                                                                                                              Oligonucleotide; DNA probe; n
             Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection.
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larity 95.2%;
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"4-4-20 WH" means the variable region of the heavy chain of the 4-4-20 mouse monoclonal antibody (Bird, R.E. et al., Science 242:423 (1988)). The number "212" refers to a specific 14-residue polypeptide linker that links the 4-4-20 WH and the CC49 VL. See Bedzyk, W.D. et al., J. Biol. Chem. 265:18615-18620 (1990). "CC49 VL" is the variable region of the light chain of the CC49 antibody, which binds to the TAG-72 antigen.

Sequence 744 BP; 199 A; 164 C; 185 G; 196 T;
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Q43288 standa
Q43288;
27-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoding a multivalent antigen-binding comprising the CC49 VL region connected through polypeptide to the 4-4-20 VH region.
Antibody; multivalent; variable region; heavy ch linker; ss.
                                         Q51746 standard; cDNA; 91 BP
Q51746;
31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
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                      SS
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                                Oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                          WO9311161-A.
10-JUN-1993.
20-NOV-1992; U09965.
25-NOV-1991; US-796936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
Synthetic.
EP-571911-A
                                                                                                                                                                                                                                                                                                                                                                                                (ENZO-) ENZON INC.
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                                                                                                                          322
                                                                                                                                   339 aggctctacttccggtagcggcaaatcttctgaaggtaaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 hvvshhhsvhhvvhhvhvvhhvvhhvhhvhyhvy 57
                                                                                                                                                                                                                                                                                                                                                                                    RE, Filpula D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACCTTCAGAAGATTTACCAGAACCAGAGGTAGAACCT 322
                                                                                                                                                                                                                                                                                                                                                                93-196999/24.
                                                                                                                        AGGTTCTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                                                                                                                                                                                                                                                     R37646.
                                                                                                                                                                              Similarity
                                                                                                                                                                     35;
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                                                                                                                                                                   66.7%;
larity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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340..381
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1..339
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1..744
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                                DNA probe; mycobacteria;
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Pred. No.
35; Misma
                                                                                                                                                                 Score 28; DB 7; I
Pred. No. 1.24e-04;
0; Mismatches 7
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No. 1.03e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy chain; light chain;
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                               disease diagnosis;
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                                                                                                                                                                   7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      Whitlow
                                                                                                                          363
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the 212 link
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QΥ
                                                    DЬ
                                                                                                                                                                                        New antigen binding proteins contg. immunoeffector or cytolytic peptide - attached to variable regions of antibody light or heavy or chain, useful in diagnosis and in destroying cancer cells Example 1; Fig 4A-B; 72pp; English.

A novel DNA construct (T29058) codes for a single-chain antigenbinding fusion protein (R97380) comprising the light chain variable region (VL) of monoclonal antibody CC49 linked to the CC49 VH region via a spacer peptide (R97379), with a C-terminal phospholipase A activating protein (PLAP) immunoeffector peptide (R97388). It was obtd. by ligating a synthetic PLAP fragment to an existing CC49/212 gene, and can be used to produce the fusion protein in transformed host cells. The fusion protein combines immunoeffector function of PLAP.

Sequence 797 BP; 196 A; 203 C; 195 G; 203 T;
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Best Local Similarity
                                                                                                    Matches
                                                                                                                            Query Match
Best Local :
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25-APR-1996;
13-OCT-1995; U12840.
13-OCT-1994; US-323445.
(ENZO-) ENZON INC.
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24-MAY-1993;
26-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 729058;
03-0CT-1996 (first entry)
CC49/CT-1996 (first entry)
CC49/CT-1996 (first entry)
CC49/CT-1996 (first entry)
single-chain antigen-binding fusion protein;
cytostatic; phospholipase A activating protei
therapy; monoclonal antibody; CC49; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5.A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T29058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Filpula D, Shorr WPI; 96-221949/22. P-PSDB; R97380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New oligo:nucleotide probes detection and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 samples
  322
                             339 aggctctacttccggtagcggcaaatcctctgaaggcaaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 CTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 vhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvv 49
  AGGTTCTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                 Similarity 78.6%, 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shorr R, Whitlow M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-889651
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/product=
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1..789
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                                                                                                                         57.1%;
78.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
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Pred.
31; M
                                                                                                 Score
Pred.
0; M
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of Mycobacteria nucleic aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                            24;
No.
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No. 4.10e-03
                                                                                       DB 22,
1.29e-02;
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                                                                                                                                                   Length
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  363
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                                                                                                    Indels
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VH
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                                                                                                 Gaps
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Best Local S
Matches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antigen binding proteins contg. immunoeffector or cytolytic peptide - attached to variable regions of antibody light or heavy chain, useful in diagnosis and in destroying cancer cells Disclosure; Page 39-40; 72pp; English.

A novel DNA construct (729059) codes for a single-chain antigen binding fusion protein (R97381) comprising the light chain variable region (VL) of monoclonal antibody CC49 linked to the CC49 VH region via a spacer peptide (R97379) and with an N-terminal phospholipase A activating protein (PLAP) immunoeffector peptide (R97368). It can be used to produce the fusion protein in transformed host cells. The fusion protein combines the tumour antigen-binding capability of CC49 with the immunoeffector function of PLAP.
            cds
                                              cds
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                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                           Q43291 standard; DNA; 1460 BP.
Q43291;
27-SEP-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-1996 (first entry)
Plap CC49/212 SCA DNA construct.
Single chain antigen-binding fusion protein; SCA; immunoeffector; cytostatic; phospholipase A activating protein; PLAP; cancer; therapy; monoclonal antibody; CC49; ds.
                                                                                cds
                                                                                                                  cds
                                                                                                                                                     cds
                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                        Antibody; multivalent; variable region; heavy chain; light chain;
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Filpula D. Shorr R. Whitlow M;
WPI: 96-221949/22.
P-PSDB; R97381.
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25-APR-1996.
13-OCT-1995; U12840.
13-OCT-1994; US-323445.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                inker;
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Similarity 78.6%;
33; Conservative
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375..426
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340..374
                                                                   /product= CC49 \
427..1065
  /r.ag= f
/product= 212 linker
1108..1449
/*+>~~
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1..795
/*tag= a
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/product= CC49 VL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 A;
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Pred. No. 1.29e-02;
0; Mismatches 9;
                                                                                           ΥH
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10-JUN-1993.
20-NOV-1992; U09965.
25-NOV-1991; US-796936.
(ENZO-) ENZON INC.
Bird RE, Filpula D, Ha
Wood JF;
WPI; 93-19699/24.
                                                                                                                      New multivalent antigen-binding protein e.g. contg. CC49 Mab regions - useful in diagnosis, for destroying blood clots and targetting cytotoxic agents or enzymes to tumour cells Example; Fig 16A; 118pp; English.

The number 212 refers to a 14-residue linker. CC49 is the CC49
                                                                                                                                                                     P-PSDB; R37649.
New multivalent antigen-binding
                                                                                                Sequence
                                                                                                            antibody.
               339 aggctctacttccggtagcggcaaatcctctgaaggcaaagg 380
  322 AGGTTCTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG 363
                                             57.1%;
Similarity 78.6%;
33; Conservet
                                                                                                  1460 BP;
                                                                                                                                                                                                                                                                                              /product= CC49 VH
                                                                                                                                                                                                                       Hardman K,
                                                                                                363 A;
                                                             Score 24; DB 7; I
Pred. No. 1.29e-02;
                                                 0
                                                 Mismatches
                                                                                                364 C;
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                                                                        Length 1460;
                                                 9; Indels
                                                                                                e;
                                                                                                                                                                                                                       Whitlow
                                                                                                                                                           CC49 Mab
                                                                                                368 T;
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Search completed: Sat Jan 9 17:20:55 1999 Job time: 25 secs.

20 47.6 25.2 12 AA7.54459 97.N1787 Rice 20 47.6 25.2 12 AA7.54459 97.N1787 Rice 3 20 47.6 477 11 AA708932 2164G01.s1 Soa 4 19 45.2 217 16 H41340 mc35f03.r1 Soa 6 19 45.2 247 12 AA7.54458 97.N1784 Rice 7 19 45.2 247 12 AA7.54458 97.N1784 Rice 8 19 45.2 259 7 HUM184D07B Human fetal br 19 45.2 363 28 AQ134058 HS_3056_A1_B09 19 45.2 363 28 AQ134058 HS_1063-B2-B01 19 45.2 411 26 B46365 HS-1063-B2-B01 19 45.2 410 16 H10208 ym02d08.s1 Hom 2 19 45.2 449 23 AA104834 mp40f09.r1 Bar 19 45.2 473 7 AA4444530 ve74h09.r1 Soa	results predicted by chance to the score of the result k of the total score distribution SUMMARIES Description	ics: Mean 7.811; Variance 1.736; scale 4.498	Database: emb1-est55 1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3 Database: genbank-est107 5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 : 10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est16 13:gb_est16 13:gb_est19 16:gb_est21 11:gb_est21 11:gb_est21 11:gb_est3 20:gb_est2 21:gb_est3 21:gb_est3 20:gb_est4 21:gb_est3 21:gb_est4 21:gb_est3 21:gb_est3 21:gb_est3 21:gb_est4 21:gb_est3 21:gb_est3 21:gb_est3 21:gb_est4 21:gb_est3 21:gb_est4 21:gb_est3 21:gb_est4 21:gb_est3 21:gb_est4 21:gb_est5 21:	Post-processing: Minimum Match 0% Listing first 45 summaries	Searched: 2275026 seqs, 895388244 bases x 2	Nmatch STD: Dbase 0; Query 0	Scoring table: TABLE default Gap 6	Title: >US-08-704-178-1 Description: (322-363) from US08704178.seq (4 of 4) Perfect Score: 42 N.A. Sequence: 322 AGGITCTACCICTGGITCIGGIAAATCITCIGAAGGIAAAGG Comp: TCCAAGATGGAGACCAAGACCATTTAGAAGACTTCCATTTCC	MPsrch_nn n.a n.a. database search, using Smith-Waterman Run on: Sat Jan 9 17:13:00 1999; Maspar time 105.04 716.018 Million ce:	Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd	
sequ 6.51e ture 6.51e preg 6.51e preg 6.51e preg 6.51e preg 1.05e ture 1.05e clize 1.05e clize 1.05e abi 1.05e pien 1.05e pien 1.05e pien 1.05e pien 1.05e	to have a being printed, tion.		12 9:gb_est13 b_est10 est5 22:gb_est6 est5 22:gb_gss2			•		ATTTCC	nan algorithm 04 Seconds cell updates/sec	n Unit. J.K.	

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MBAFCW/F03F3 Brug1a ma nbxb0013L05r CUGI Rice nbxb0006G12f CUGI Rice BSBmMFSZ01L5SK Brug1a Homo sapiens ntcon6 co BSBmMFSZ07D5SK Brug1a	3D6AAZE10T3 Brugj 48g10.r1 Soares ; 112f02.x1 Soares n 37a03.r1 Soares n 96f08.s1 Stratage	3h05.r1 soare 7h06.x1 NCI_C 7h12.x1 NCI_C 3073_A2_B05_M	14a03.s1 _2064_A1_ BmMFSZ05N BmMFSZ05N 43a10.r1 43a10.r1 AFCZ7A01T	65e02.rl Soares N Ov3MCA654SK Onchc AFCE0B07T3 Brugia 91f01.sl Homo sap	tRHI brij pie pie -23 -23
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ALIGNMENTS

Query Match Best Local Matches	SOUTCE BASE COUNT ORIGIN	FEATURES	COMMENT	AUTHORS TITLE JOURNAL	ORGANISM	ACCESSION NID KEYWORDS SOURCE	RESULT 1 LOCUS DEFINITION
Query Match 47.6%; Score 20; DB 27; Length 243; Best Local Similarity 85.2%; Pred. No. 6.51e-05; Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	1243 /organism="Fugu rubripes" /db_xref="taxon:31033" /clone_lib="cosmid 184G17" /clone="184G17aD8" 38 a 71 c 33 g 93 t 8 others	<pre>V_type: phagemid PRIMER: KS DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence. Location/Qualifiers</pre>	CB10 1SB, UK. Email:	Elgar, G. Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y., Williams, G. and Brenner, S. Direct Submission Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource	Fugu rubripes Fugu rubripes Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Meopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.	sequence. AL030157 g3272271 GSS; genome survey sequence. Fugn rubrines	FR0033790 243 bp DNA GSS 27-JUN-1998 Fugu rubripes GSS sequence, clone 184G17aD8, genomic survey

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RESULT 2
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Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S
                                                                                                                                                                             z164d01.s1
506689 3',
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Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Schee, M.C. and Eun, M.Y.
Large-scale Sequencing Analysis of ESTs from Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence.
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                                                                                                      human.
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Embryophyta; Tracheophyta;
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/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: Eco:
XhoI: Directional cDNA library inserted into
xhoI: S'end with EcoRI and 3' end with X'
vector at 5'end with EcoRI and 3' end with X'
/db_xref="faxon:4530"
/clone="97SN1787"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
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6.51e-05;
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A45036 PUR
                                                      midbrain, pons and
                                                                                                                                                                                                                                                                                                                              55-year old male. 1st oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens clone=175801 library=Soares adult brain N2b5HB55Y vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800 Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
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larity 88.5%;
Conservative
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/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I
Site_2: Eco RI; 1st strand cDNA was primed with a Not
oligo(dT) primer [5'
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/lab_host="DH10B"
88 c 96 g
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/clone="506689"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 bp mRNA EST 31-JUL-1995 Homo sapiens cDNA clone 175801 5' similar to SP:A45036 ALPHA=SINGLE-STRANDED-DNA-BINDING PROTEIN - ;.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mc35f03.r1 Soares
5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University Scho 4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 217)
                                                                                             Contact: Marra M/MOUSE EST Project
WashUrHHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                Waterston, R.
The WashU-HHMI Mouse
                                                                                                                                                                                                                                                                       1 (bases 1 to 229)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W35023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; mage consortium (info@image.llnl.gov) for further i Trace considered overall poor quality Possible reversed clone: similarity on wrong strand.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
WashU-Merck EST Project
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                                                                            Tel: 314 286 1800
                                                                                                                                                                                              Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Source: IMAGE Consortium, LINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
                                                              Fax: 314 286 1810
                                                                                                                                                                                                                                                        Theising, B., Wylie, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                      Email: mouseest@watson.wustl.edu
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/clone="175801"
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                                                                                                                                                                                                                                                      Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p3NMF19.5 Mus musculus cDNA clone 350525
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Cytogenetics National Inst. of Agri. Sci. Suwon, Kyunggido, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nahm, B.H., Kim, J.K., Kim, W.Y., Y Kim, W.T., Kim, W.Y., Y Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa
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                                                                                                                                                                                                                                                                                                                           Email: myeun@sun20.asti.re.kr
Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse_Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suwon, Kyunggido, Ko
Tel: 82 331 290 0301
Fax: 82 331 290 0307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poales;
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larity 77.1%;
Conservative
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                                                                 /organism="Oryza sativa"
/organism="Milyang23"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI: Site_2:
/note="Vector: pBluescript SK(+); Site_1 into lambda ZAPI
XhoI; Directional cDNA library inserted into lambda ZAPI
XhoI; Oresional with EcoRI and 3' end with Xho I site."
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/db_xref="taxon:10090"
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/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resist
                           vector at 5'end with EcoRI and /db_xref="taxon:4530" /clone="97SN1784"
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/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19; DB 21;
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CTACCTCTGGTTCTGGTAAATCTTCTGAAGGTAAAGG 363
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Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho
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771-01
       Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co.,Ltd: 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:0886-65-2888, Fax:0886-37-1035) submitted (30-May-1995) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takalohi,A., Takada,S., watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y. Unpublished(101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
2 (bases 1 to 259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
.vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens cDNA to mRNA, clone_lib:Clontech human fetal brain polyA+ mRNA (#6535).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST: EST(expressed sequence tag); Human fetal brain; similar none(May 29,1995).
                                                                                                                                                                                                                                                                                                                                                                                                         Phone: 0886-65-2888
Fax : 0886-37-1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                             Similarity 22; Conser
JOS 337 bp mRNA musculus fertilized egg cDNA 3'-end
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fetal brain cDNA 5'-end GEN-184D07,
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                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Clontech human fetal brain polyA+ mRNA
(#6535)"
35 c 45 g 80 t 26 others
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/dev_stage="5 days after pollination"
/lab_host="E. coli SOLE"
/lab_host="E. 21 g 34 t 169 ot
                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                             45.2%;
                                                                                                                                                                         Score 19; DB 7; 1
Pred. No. 1.05e-03
6; Mismatches
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Pred. No. 1.05e-03;
22; Mismatches 9
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                                                                                                                                                                                                               Length 259
 sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 CCCTTACTTTAAAAATATTTCCCAGAACCACGGGT 262
                                    High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seatt Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
AQ134058
g3525424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ134058 363 bp
HS_3056_A1_B09_MR CIT
sapiens genomic clone
                                                                                                                                                                                                                                                         1 (bases 1 to 363)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Shaker,R., Schmidt,S., Traicoff,R. and Hood,L.E. Construction of a Characterized Clone Resource for Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-JAN-1998) to the DDBJ/EMBL/GenBank databases. Hirofumi Doi, Doi Bioasymmetry Project, ERATO, Japan Science and Technology Corporation (JST); WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba-shi, Chiba 261-7112, Japan (E-mail:hddbioa.jst.go.jp, Tel:81-43-299-1351, Fax:81-43-297-7530) Location/Qualifiers
Sequence Tagged Connector Plate: 3056 row: C colu
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS.
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Unpublished (1998)
2 (bases 1 to 337)
Doi,H. and Ko,M.S.H.
Direct Submission
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                                                                                                                                                                          Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                     Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.2%;
Similarity 77.1%;
27; Conservation
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Mus musculus (strain:C57BL/6J) fertilized one-cell-emm
mRNA, clone_lib:Mouse fertilized one-cell-embryo cDNA
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C87905
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DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Paonessa,P.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Mouse fertilized one-cell-embryo/dev_stage="fertilized one-cell-embryo" 86 c 90 g 93 t 1 others
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/clone="J0253E04"
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/strain="C57BL/6J"
  column: 17
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Pred. No. 1.05e-03;
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                                                                                                            WA 98109, USA
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                316 GTGCTACCTCTGGTCCTTCTAACTCTTCT 344
 324
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g2551199
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HS-1063-B2-B01-MF.abi
sapiens genomic clone
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High quality sequence stop
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1 (bases 1 to 411)
                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Zackrone KD,
University of Washington
Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E. Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                   Email: kzackron@u.washington.edu
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(206) 685-7301
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                                                       45.2%;
larity 82.8%;
Conservative
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larity 80.6%;
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1 47 c
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones
E-Coli DH10B"
                                                                                                                             /sex="M"
91 c
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E-Coli DH10B"
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/clone="Plate=CT 796 Col=2 Row=D"
/clone_lib="CIT Human Genomic Spe
                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                         325 TICTACCICTGGITCTGGTAAAICTICTGAAGGTA 359
                                                                                                                                                                                                                                                                     198 TTCAACCCCTGGTTGTGGCACAACTTTTCAAGGTA 232
                                                                                                                                                                                                                                                                                                  Local Similarity res 27; Conser
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EST.
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, Holman, M., Kucaba, T., Le, M., Lennon, G., Man Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                  AA104834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
WashU_Merck EST project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H10208 430 bp mRNA EST ym02d08.sl Homo sapiens cDNA clone 46914 3'.
1 (bases 1 to 449)
Marra, M., Hillier, L.,
                               Mus
                                           Eukaryotae;
Vertebrata;
                                                                         house mouse.
Mus musculus
                                                                                                                                                                mp40f09.rl Barstead
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Source: IMAGE Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stops:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDB: G00-419-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/clone="46914"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                45.2%;
77.1%;
                                         mitochondrial eukaryotes; Metazoa; Eutheria; Rodentia; Sciurognathi; I
                                                                                                                                                                                                                                                                                                                                                                                                                         .430
                                                                                                                                                                                                                                                                                                                                                                           101 c
                                                                                                                                                                            449 bp
                                                                                                                                                                MPLRB1 Mus musculus
                                                                                                                                                                                                                                                                                                                Score 19; DB 16;
Pred. No. 1.05e-03;
 Allen, M.,
                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                          70 g
                                                                                                                                                                               mRNA
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 Bowles, M.,
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                                                                                                                                                                cDNA clone
                                                                                                                                                                                                                                                                                                                              Length 430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                           1 others
Dietrich, N., Dubuque, T.,
                                                                                                                                                                                                                                                                                                  Indels
                                           ; Chordata;
Muridae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hawkins, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,G., Marra,M.,
                                                                                                                                                              13-FEB-1997
: 571721 5',
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                                             Murinae;
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mRNA
BASE COUNT
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                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                     327
                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Mur: Wurinae; Mus.

1 (bases 1 to 473)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                 AA444530 473 bp mrNA EST U3-JUN-199/
ve74h09.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone
832001 5' similar to gb.x58380 M.musculus HMGI-C mRNA for a nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -zomij zc. - 414.
High quality sequence stop: 414.
Location/Qualifiers
            Unpublished (1996)
                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                           g2157470
                                                                                                                                                                                                                                                                             phosphoprotein
AA444530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashIn-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                The WashU-HHMI Mouse
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                                                                                                                                                                                                                          house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 45.2%;
Similarity 77.1%;
27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer: -28ml3 rev2 ET from Amersham
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Kidney"
/dev_stage="6 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Barstead MPLRB1"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="BALB/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .>449
134 c
                                                                                                                                                                                                                                                                                           (MOUSE);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19; DB 23;
Pred. No. 1.05e-03;
0; Mismatches 8
                              EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 g
                                                                                                                                                                                                                                                                                           mRNA sequence
                                                                                                                 Bowles, M., Dietrich, N., Dubuque, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 CCTTCAGAAGATTTACCAGAACCAGAGGTAGAA 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 CCTTCAGAAGATCCATCTGATGCTGAGGTAGAA 41
          Gilbert Biology, Stanford, CA 94305
Tel: 650 723 3232
Fax: 650 725 8309
Email: fa.srl@forsythe.stanford.edu
                                                                                                                                                                           Covitz,P.A., Smith,L.S. and Long,S.R. Expressed sequence tags from a root h truncatula cDNA library
                                                                                                           Contact: Long SR
Department of Biological
                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                        Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; vascular plants; seed plants; Magnoliophyta;
Magnoliopsida; Rutanae; Sapindales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                          barrel medic.
Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                 AA660633 588 bp mRNA EST 00521 MtRHE Medicago truncatula cDNA 5' similar to
                                                                                Stanford University
                                                                                                                                                                                                                                                                                                                                                                          AA660633
                                                                                                                                                                                                                                                                                                                                                                                         dihydroflavonol-4-reductase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
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4444 Forest Park Parkway, Box 8501, St. La
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Fax: 314 286 1810
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                                                                                               Institute
                                                                                                                                                                                                                          (bases 1 to 588)
primer: T3
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h quality sequence stop: 335.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="4 weeks"
/lab_host="DH10B"
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/clone="832001"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares mouse
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156 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 7; I
Pred. No. 1.05e-03;
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                                                                                                              Sciences and
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                                                               94305-5020,
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RESULT 15
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Best Local Similarity 74.4%;
Matches 29; Conservative
                                                                                                                                  Query Match 45.2%;
Best Local Similarity 85.2%;
Matches 23; Conservative
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                                    195 TICTICCTCTGGTTCTGAAACATCTTC 221
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325 TTCTACCTCTGGTTCTGGTAAATCTTC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fugu rubripes
Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
Repoterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
1 (bases 1 to 619)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
AL030199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        One pass dye-terminator sequencing of cosmid cloned genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS; genome survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                 /organism="Fugu rubripes"
/ob_xref="taxon.31033"
/clone_lib="cosmid 184G17"
/clone="184G17bF10"
a 157 c 97 g 213 t
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/cultivar="Jemalong"
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